
[WIRE] [PULSE] [SIGNAL] [ALPHA] [BETA] [GAMMA] [DELTA] [Epsilon] [Zeta] [Eta] [Theta] [Iota] [Kappa] [Lambda] [Mu] [Nu] [Xi] [Omicron] [Pi] [Rho] [Sigma] [Tau] [Upsilon] [Phi] [Chi] [Psi] [Omega] [TW]

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MPsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Feb 19 10:18:15 1998; Maspar time 190.35 Seconds
767.414 Million cell updates/sec
***** output not generated.

File: >US-08-910-733-12
Description: (1-579) from US08910733.seq
Perfect Score: 579
N.A. Sequence: 1 CAGAAGACCTCTGCTCTA.....TCCAGGAGGAGGAGTAGTAC 579
Comp: GTCTCTCTGGAGGACAGGAT.....AGGTCCTCTGCTCATCATG

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 333433 seqs, 126143548 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: STS
1:STS1 2:STS2 3:STS3 4:STS4 5:STS5 6:STS6 7:STS7 8:STS8
9:STS9 10:STS10 11:STS11 12:STS12 13:STS13 14:STS14
15:STS15 16:STS16 17:STS17 18:STS18 19:STS19 20:STS20
21:STS21 22:STS22 23:STS23 24:STS24 25:STS25 26:STS26 27:STS27
28:STS28 29:STS29 30:STS30 31:STS31 32:STS32 33:STS33 34:STS34
35:STS35 36:STS36 37:STS37 38:STS38 39:STS39 40:STS40
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65:STS65 66:STS66 67:STS67 68:STS68 69:STS69 70:STS70
71:STS71 72:STS72 73:STS73 74:STS74 75:STS75 76:STS76
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83:STS83 84:STS84 85:STS85 86:STS86 87:STS87 88:STS88
89:STS89 90:STS90 91:STS91 92:STS92 93:STS93 94:STS94
95:STS95 96:STS96

Statistics: Mean 10.575; Variance 2.175; scale 4.863
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result	Query			
No.	Score	Match	Length	DB ID Description Pred. No.
1	26	4.5	239	94 RNU17366 Rattus norvegicus pol 8.14e-09
2	26	4.5	239	45 RNU17366 Rattus norvegicus pol 8.14e-09

3	26	4.5	239	13	RNU17366	Rattus norvegicus pol	8.14e-09
4	25	4.3	287	13	HUMUT7023	Human STS UT7023	1.50e-07
5	25	4.3	374	70	HS1301667	nh44e07.s1 NCI_CGAP_P	1.50e-07
6	25	4.3	374	38	AA506215	nh44e07.s1 NCI_CGAP_P	1.50e-07
7	25	4.3	400	6	G18033	human STS SHGC-8829 C	1.50e-07
8	25	4.3	431	4	G09397	human STS CHLC-CC110	1.50e-07
9	25	4.3	555	4	G09540	human STS CHLC-CC110	1.50e-07
10	24	4.1	307	17	N60626	TgESTzy20h10.r1 TgrH	2.54e-06
11	24	4.1	387	92	TG626	TgESTzy20h10.r1 TgrH	2.54e-06
12	24	4.1	387	10	HS2682D9	H. sapiens (D5S630) D	2.54e-06
13	24	4.1	400	4	G11022	human STS SHGC-8495 C	2.54e-06
14	24	4.1	429	4	G09443	human STS CHLC-CC11.P	2.54e-06
15	24	4.1	532	13	HUMUT1002	human STS UT1002	2.54e-06
16	24	4.1	557	42	AA524678	nh35g06.s1 NCI_CGAP_P	2.54e-06
17	24	4.1	557	72	HS1316357	nh35g06.s1 NCI_CGAP_P	2.54e-06
18	23	4.0	142	13	HUMUT6693B	Human STS UT6693, 3'	3.97e-05
19	23	4.0	162	13	HUMUT49A	Human STS UT49, 5' pr	3.97e-05
20	23	4.0	174	13	HUMUT5072A	Human STS UT5072, 5'	3.97e-05
21	23	4.0	236	13	HUMUT6693A	Human STS UT6693, 5'	3.97e-05
22	23	4.0	272	81	MML1243272	vg57g05.r1 Beddington	3.97e-05
23	23	4.0	302	13	HUMUT5309B	Human STS UT5309, 3'	3.97e-05
24	23	4.0	330	90	OSI1213A	Rice cDNA, partial seq	3.97e-05
25	23	4.0	331	90	OSI1058A	Rice cDNA, partial seq	3.97e-05
26	23	4.0	354	54	HS1206473	zv29g09.r1 Soares ova	3.97e-05
27	23	4.0	406	96	MML140152	mw11b02.r1 Soares mou	3.97e-05
28	23	4.0	418	13	HUMUT1548	Human STS UT1548	3.97e-05
29	23	4.0	428	15	AA236110	zs05e11.r1 NCI_CGAP_G	3.97e-05
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31	23	4.0	491	73	HS1322990	nj68l11.s1 NCI_CGAP_P	3.97e-05
32	23	4.0	531	89	MAA29866	vj13d11.r1 Barstead m	3.97e-05
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35	23	4.0	569	41	AA521142	aa73b02.s1 NCI_CGAP_G	3.97e-05
36	23	4.0	588	4	G09471	human STS CHLC-ATC5A0	3.97e-05
37	23	4.0	780	47	DMAA91050	LD09995.5prime LD Dro	3.97e-05
38	22	3.8	184	18	W35518	TgESTzy90e08.r1 TgrH	5.66e-04
39	22	3.8	353	59	HS1241401	zx74a01.s1 Soares ova	5.66e-04
40	22	3.8	460	10	HS094XB3	H. sapiens (D2S2360) D	5.66e-04
41	22	3.8	481	68	HS1289285	ab01h08.r1 Stratagene	5.66e-04
42	22	3.8	485	77	HSA446141	zw64a05.r1 Soares tes	5.66e-04
43	22	3.8	528	31	AA489827	ab04i05.s1 Stratagene	5.66e-04
44	22	3.8	556	47	DMAA39252	LD13764.5prime LD Dro	5.66e-04
45	22	3.8	656	48	DMAA92382	LD11235.5prime LD Dro	5.66e-04

ALIGNMENTS

RESULT 1
ID RNU17366 standard; DNA; STS; 239 BP.
AC U17366;
NI 9603167
DT 23-DEC-1994 (Rel. 42, Created)
DE Rattus norvegicus polimeric immunoglobulin receptor (PIGR-Forml)
DE gene, 3'UTR, microsatellite.
DE microsatellite; STS.
KW Rattus norvegicus (Norway rat)
OC Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
OC Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
OC Murinae; Rattus.
RP 1-239
RP MEDLINE: 93315123
RA Koch K.S., Fletcher R.G., Grond M.P., Leffert H.L.;
RT 'A 43-base-pair complementary DNA sequence homology and triplet
RT repeat motif among putative polymorphic immunoglobulin receptor
RT messenger RNAs in regenerating rat liver [letter];
RL Hepatology 18:226-228(1993).
RN [2]
RP 1-239
RP MEDLINE: 95258315.
RA Koch K.S., Gleiberman A.S., Aoki T., Leffert H.L., Feren A.,
RA Jones A.L., Fodor E.J.;

FT	/evidence=EXPERIMENTAL
FT	/rpt_family="trinucleotide"
FT	/label=GGA_GAA_repeats
FT	28..179
FT	/gene="PIGR-Forml"
FT	/note="1 of 2 PCR product subclones. Unlike F2 (GenBank
FT	Accession No. U17367), GGA and GAA tracts are longer and
FT	shorter; d[AA] and ATAGAA junctions are seen."
FT	/replace=""
FT	repeat_region
FT	64..173
FT	/note="contains 36 GAA triplets; a dinucleotide (d[AA]) at
FT	nts 79-80 interrupts the 5th and 6th GAA repeat unit; a
FT	similar interruption occurs in Wistar genomic clone
FT	Lambda2IGR (GenBank Accession Number U08273)."
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FT	/evidence=EXPERIMENTAL
FT	/rpt_family="trinucleotide"
FT	/rpt_unit=GAA-repeat
FT	174..179
FT	/gene="PIGR-Forml"
FT	/note="separates upstream STMSS from a 283 bp 'unit'
FT	(starting here at nt 180) in the 3'UTRs of Fisher rat Grou
P	
FT	1 cDNAs and Wistar rat genomic clone Lambda2IGR (GenBank
FT	Accession No. U08273); absent from F2."
FT	/evidence=EXPERIMENTAL
FT	/label=ATAGAA-junction
FT	misc_feature
FT	180...239
FT	/gene="PIGR-Forml"
FT	/note="sequence match to GenBank Accession Numbers U08273,
FT	U07886 and U02506; Group 2 pig-R cDNAs lack this unit
FT	(GenBank Accession Numbers L22660, U01145, U00762 and
FT	U00763)."
FT	/evidence=EXPERIMENTAL
FT	complement(221..239)
FT	/gene="PIGR-Forml"
FT	/note="primers were from regions flanking STMSS in Fisher
FT	ratt group 1 pig-R cDNAs (GenBank Accession Numbers U02506,
FT	U07886)."
FT	Sequence 239 BP; 120 A; 14 C; 87 G; 18 T; 0 other;
SQ	
	Query Match 4.5%; Score 26; DB 94; Length 239;
	Best Local Similarity 73.2%; Pred. No. 8.14e-09;
	Matches 41; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
Ddb	33 aggagaggagagagagggaggaggaggaagaagaagaagaagaagaaga 88
QY	57 AGAAGGAGGTGGAGGAGGAGGAGGAGGTGAACACACTGTCTCAAGGAGACGA 112
RESULT	2
LOCUS	RNU17366 239 bp DNA STS 26-JUN-1997
DEFINITION	Rattus norvegicus polymeric immunoglobulin receptor (PIGR-Forml)
	gene, 3'UTR, microsatellite.
ACCESSION	U17366
NID	G603167
KEYWORDS	STS; microsatellite.
SOURCE	Rattus norvegicus
ORGANISM	Norway rat.
	Rattus norvegicus
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
	Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
	Murinae; Rattus
REFERENCE	1 (bases 1 to 239)
AUTHORS	Koch,K.S., Fletcher,R.G., Grond,M.P. and Leffert,H.L.
TITLE	A 43-base-pair complementary DNA sequence homology and triplet
	repeat motif among putative polymeric immunoglobulin receptor
	messenger RNAs in regenerating rat liver
JOURNAL	Hepatology 18 (1), 226-228 (1993)
MEDLINE	93315123
REFERENCE	2 (bases 1 to 239)
AUTHORS	Koch,K.S., Gleiberman,A.S., Aoki,T., Leffert,H.L., Feren,A.,
TITLE	Jones,A.L. and Fodor,E.J.
	Discrepant expression and variable numbers of neighboring GGA-
	and

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	repeat_region	/gene="PIGR-Forml"					
		/note="#1 of 2 PCR product subclones. Unlike F2 (GenBank Accession No. U17367), GGA and GAA tracts are longer and shorter; d[AA] and ATAGAA junctions are seen."					
		/replace=""					
		64..173					
		/note#"contains 36 GAA triplets; a dinucleotide (d[AA]) at nts 79-80 interrupts the 5th and 6th GAA repeat unit; a similar interruption occurs in Wistar genomic clone Lambda2igr (GenBank Accession Number U08273)."					
		/rpt_type=tandem					
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		/note#"separates upstream STMSS from a 283 bp 'unit' (starting here at nt 180) in the 3'UTRs of Fisher rat group 1 cDNAs and Wistar rat genomic clone Lambda2igr (GenBank Accession No. U08273); absent from F2."					
		/evidence=experimental					
		/label=ATAGAA-junction					
		180..239					
		/gene="PIGR-Forml"					
		/note#"sequence match to GenBank Accession Numbers U08273, U07886 and U02506; Group 2 pig-R cDNAS lack this unit (GenBank Accession Numbers L22660, U01145, U00762 and U00763).					
		/evidence=experimental					
		complement(221..239)					
		/gene="PIGR-Forml"					
		/note#"primers were from regions flanking STMSS in Fisher rat Group 1 pig-R cDNAS (GenBank Accession Numbers U02506, U07886)."					
		BASE COUNT 120 a 14 c 87 g 18 t					
	ORIGIN						
		Query Match 4.5%; Score 26; DB 45; Length 239;					
		Best Local Similarity 73.2%; Pred. No. 8.14e-09;					
		Matches 41; Conservative 0; Mismatches 15; Indels 0; Gaps 0;					
Ddb	33 aggaggagggaggaggaggaggaggaggagaagaagaagaagaagaagaaga 88 QQ	57 AGAAGGAGGTGGAGGAGGAGGAGAAGTCAACACAATCTGCATCAAAGGACGCGA 112					
RESULT 3	RNU17366	239 bp DNA	STS	18-MAY-1995			
	Locus	Rattus norvegicus polymeric immunoglobulin receptor (PIGR-Forml)					
	DEFINITION	gene, 3'UTR, microsatellite.					
	ACCSSION	U17366					
	NID	9603167					
	KEYWORDS	STS; microsatellite.					
	SOURCE	ratt. rat.					
	ORGANISM	Rattus norvegicus					
		Eukaryotes; mitochondrial eukaryotes; Metazoa: Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.					
		1 (bases 1 to 239) Koch,K.S., Gleiberman,A.S., Aoki,T., Leffert,H.L., Feren,A., Jones,A.L. and Fodor,E.J.					
	TITLE	Discordant expression and variable numbers of neighboring GGA- and GAA-rich triplet repeats in the 3' untranslated regions of two groups of messenger RNAs encoded by the rat polymeric immunoglobulin receptor gene					
JOURNAL	MEDLINE	Nucleic Acids Res. 23 (7), 1098-1112 (1995)					
	REFERENCE	95258315					
AUTHORS		2 (bases 1 to 239) Leffert,H.L.					
	TITLE	Direct Submission					
JOURNAL		Submitted (18-NOV-1994) Hyam L. Leffert, Pharmacology/Center Molecular Genetics, University of California at San Diego. Basic					

Science Building Room 3025, La Jolla, CA 92093-0636, USA
 Location/Qualifiers
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 /organism="Rattus norvegicus"
 /strain="Fisher 344"
 /note="F1 (1 of 2 genomic subclones obtained by PCR; the 2nd is F2)"
 /clone="pBluescriptIIKS(-)F1"
 /sex="male"
 /cell_type="hepatocyte"
 /tissue_type="liver"
 /dev_stage="adult"
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 /gene="PIGR-Form1"
 1..239
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 /gene="PIGR-Form1"
 /note="agarose gel purified PCR product subcloned into pBS"
 label=triplet_repeat
 1..19
 /gene="PIGR-Form1"
 /note="primers were from regions flanking STMSS in Fisher rat Group 1 pig-R cDNAs (GenBank Accession Numbers U07506, U07886)."
 1..18
 /gene="PIGR-Form1"
 /note="sequence match to GenBank Accession Numbers L22660, U00762, U00763, U01145, U07886 and U02506."
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 19..63
 /note="GGA tract size of F1 > F2 but is - to GGA tract size in Wistar rat genomic clone Lambda21gr (GenBank Accession No. U08273); all genomic GGA tracts are < GGA tract sizes in all Fisher rat pig-R cDNAs."
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 /evidence=experimental
 /rpt_family="trinucleotide"
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 /gene="PIGR-Form1"
 /standard_name="microsatellite"
 /note="contains 2 dissimilar triplet repeats (GGA[n=15], GAA[n=36]) represented discordantly in Fisher Group 1 cDNAs (GenBank Accession Numbers U02506, U07886) and U00762 (GenBank Accession Numbers L22660, U01145, U00762 and U00763); this region putatively contains at least one S1 nuclease-sensitive site and potentially may be capable of forming non-B, triplex or tetraplex structure"
 /rpt_type=tandem
 /evidence=experimental
 /rpt_family="trinucleotide"
 /label=GGA_GAA_repeats
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 /gene="PIGR-Form1"
 /note="1 of 2 PCR product subclones. Unlike F2 (GenBank Accession No. U17367), GGA and GAA tracts are longer and shorter; d[AA] and ATAGAA junctions are seen."
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 /note="contains 36 GAA triplets; a dinucleotide (d[AA]) at nts 79-80 interrupts the 5th and 6th GAA repeat unit; a similar interruption occurs in Wistar genomic clone Lambda21gr (GenBank Accession Number U08273)."
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 /rpt_unit=GAA-repeat
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FEATURES
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 primer_bind
 STS
 gene
 primer_bind
 STS
 primer_bind
 misc_feature
 repeat_region
 satellite
 allele
 repeat_region
 misc_feature

Science Building Room 3025, La Jolla, CA 92093-0636, USA
 Location/Qualifiers
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 /organism="Rattus norvegicus"
 /strain="Fisher 344"
 /note="F1 (1 of 2 genomic subclones obtained by PCR; the 2nd is F2)"
 /clone="pBluescriptIIKS(-)F1"
 /sex="male"
 /cell_type="hepatocyte"
 /tissue_type="liver"
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 /gene="PIGR-Form1"
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 /note="agarose gel purified PCR product subcloned into pBS"
 label=triplet_repeat
 1..19
 /gene="PIGR-Form1"
 /note="primers were from regions flanking STMSS in Fisher rat Group 1 pig-R cDNAs (GenBank Accession Numbers U02506, U07886)."
 1..18
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 /note="sequence match to GenBank Accession Numbers L22660, U00762, U00763, U01145, U07886 and U02506."
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 label=CA-rich_region
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 /note="GGA tract size of F1 > F2 but is - to GGA tract size in Wistar rat genomic clone Lambda21gr (GenBank Accession No. U08273); all genomic GGA tracts are < GGA tract sizes in all Fisher rat pig-R cDNAs."
 /rpt_type=GGA-repeat
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 /gene="PIGR-Form1"
 /standard_name="microsatellite"
 /note="contains 2 dissimilar triplet repeats (GGA[n=15], GAA[n=36]) represented discordantly in Fisher Group 1 cDNAs (GenBank Accession Numbers U02506, U07886) and U00762 (GenBank Accession Numbers L22660, U01145, U00762 and U00763); this region putatively contains at least one S1 nuclease-sensitive site and potentially may be capable of forming non-B, triplex or tetraplex structure"
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 /evidence=experimental
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 /label=GGA_GAA_repeats
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 /gene="PIGR-Form1"
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 /note="contains 36 GAA triplets; a dinucleotide (d[AA]) at nts 79-80 interrupts the 5th and 6th GAA repeat unit; a similar interruption occurs in Wistar genomic clone Lambda21gr (GenBank Accession Number U08273)."
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FEATURES
 source
 primer_bind
 STS
 gene
 primer_bind
 STS
 primer_bind
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 satellite
 allele
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 misc_feature


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BASE COUNT      90 a      38 c      101 g      54 t      4 others
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Query Match      4.3%; Score 25; DB 13; Length 287;
Best Local Similarity 93.1%; Pred. No. 1.50e-07;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 80 gaagaaggagtgaggagtgaggagggg 108
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QY 55 GAAGAAGGAGGTGGAGGAGGAGGAGGAGG 83

RESULT 5
ID HS1301667 standard; RNA; EST; 374 BP.
AC AA506215;
NI 92242455
DT 04-JUL-1997 (Rel. 52, Created)
DT 12-JUL-1997 (Rel. 52, Last updated, Version 2)
DE nh44e07.s1 NCI_CGAP_Pr5 Homo sapiens cDNA clone 955236.
KW EST.
OS Homo sapiens (human)
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
NC 1
RP 1-374
RA NCI-CGAP;
RT "National Cancer Institute, Cancer Genome Anatomy Project (CGAP),"
RT "Tumor Gene Index";
RL Unpublished.
CC Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email:
CC Robert.Strausberg@nih.gov Tissue Procurement: David G. Bostwick,
CC M.D., Rodrigo F. Chuquiqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CC cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library
CC Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington
CC University Genome Sequencing Center Clone distribution: NCI-CGAP
CC Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html Insert
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CC Amersham High quality sequence stop: 333.
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FH epithelial cells, cDNA made by oligo-dT priming.
FH Non-directionally cloned. Size selected on agarose gel,
FH average insert size 600 bp."
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FH /sex="male"
FH /tissue_type="prostate"
FH /lab_host="DH10B"
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Best Local Similarity 90.3%; Pred. No. 1.50e-07;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 287 gaagaaggagtgaggagtgaggaggggtg 317
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QY 55 GAAGAAGGAGGTGGAGGAGGAGGAGGAGG 85

RESULT 6
LOCUS      AA506215      374 bp      mRNA      EST      10-JUL-1997
DEFINITION nh44e07.s1 NCI_CGAP_Pr5 Homo sapiens cDNA clone 955236.
ACCESSION  AA506215
NID        92242455
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens

Query Match      4.3%; Score 25; DB 70; Length 374;
Best Local Similarity 90.3%; Pred. No. 1.50e-07;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 287 gaagaaggagtgaggagtgaggaggggtg 317
|||||
QY 55 GAAGAAGGAGGTGGAGGAGGAGGAGGAGG 85

RESULT 7
LOCUS      GI8033      400 bp      DNA      STS      05-MAR-1996
DEFINITION human STS SHGC-8829 clone pG-4562.
ACCESSION  GI8033
NID        GI215459
KEYWORDS   STS sequence; primer; sequence tagged site.
SOURCE     human Plasmid clones, generated from a lymphoblastoid cell line
           from a human male. Localized to human chromosome 18 by analysis on
           the NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell
           Institute for Medical Research, Camden, NJ 08103.

ORGANISM   Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcoptrygii; Chonata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 400)
AUTHORS   Myers,R.M.
JOURNAL   Unpublished (1996)
COMMENT   Contact: Richard M. Myers
           Stanford Human Genome Center (SHGC)
           Stanford University School of Medicine
           Department of Genetics, M-344, Stanford, CA 94305, USA
           Tel: 4157259687

```

Fax: 4157259689
Email: myers@hgc.stanford.edu

Primer A: CTGCTCAATTCACCATCAGT
Primer B: GGGACAAAGAGAGAACTGG
STS size: 268
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
Annealing: 66 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30

Thermal Cycler: Perkin Elmer 9600

Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/uL
Total Vol: 10 uL

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Chromosome 18.
Location/Qualifiers
source 1..400
STS /organism="Homo sapiens"
100..367
primer_bind /map="18"
100..120
primer_bind /map="18"
complement(347...367)

BASE COUNT 110 a 75 c 92 g 120 t 3 others

Query Match 4.3%; Score 25; DB 6; Length 400;
Best Local Similarity 79.1%; Pred. No. 1.50e-07;
Matches 34; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 25 agaggtgagagagagagctattagggaatgctcagta 67
|||||
60 AGAGGTGGAGGAGGAGGAGAGGTGAGACAAATGCTGACTCA 102

RESULT 8
LOCUS G09397 431 bp DNA STS 14-AUG-1995
DEFINITION human STS CHLC.CCT10.P9317 clone CCT10.
ACCESSION G09397
NID 9941246
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from xy individual of French nationality.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1995)
COMMENT Synonyms: CCT10, CHLC.CCT10.T9316
Contact: Dr. Jeffrey C. Murray
UofI
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347

Email: jeff-murray@uiowa.edu

Primer A: GTGGCTGTGATTCACCTAC
Primer B: TCTGTGTTAGTTTTCACCA
STS size: 177
PCR Profile:

denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C
extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degrees C

Protocol:
Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Taq Polymerase: 0.3 units
Total Vol: 10 uL

Buffer:
MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3
Location/Qualifiers
source 1..431
STS /organism="Homo sapiens"
78..254
primer_bind 78..97
primer_bind complement(234..254)
BASE COUNT 142 a 61 c 127 g 95 t 6 others
ORIGIN

Query Match 4.3%; Score 25; DB 4; Length 431;
Best Local Similarity 87.9%; Pred. No. 1.50e-07;
Matches 29; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 164 aagagagagagagagagagagagagagagag 196
|||||
QY 56 AAGAAGAGGTGGAGGAGGAGGAGAGGTGAAG 88

RESULT 9
LOCUS G09540 555 bp DNA STS 14-AUG-1995
DEFINITION human STS CHLC.GCT6H01.P11096 clone GCT6H01.
ACCESSION G09540
NID 9941389
KEYWORDS STS sequence; primer; sequence tagged site.
SOURCE human vector-pJCP1 host-E.coli dut+ung+ (DH10B) Marker Selected genomic DNA prepared from xy individual of French nationality.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.
TITLE Cooperative Human Linkage Center
JOURNAL Unpublished (1995)
COMMENT Synonyms: GCT6H01, CHLC.GCT6H01.T11095
Contact: Dr. Jeffrey C. Murray
UofI
The University of Iowa
Department of Pediatrics, Iowa City, IA 52242, USA
Tel: (319) 356-3508
Fax: (319) 356-3347
Email: jeff-murray@uiowa.edu

Primer A: GAGCCTTTTGCATCTCC
Primer B: GGGTAACAGAGCAAGACCTC
STS size: 243
PCR Profile:

denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C

extension: 15 seconds at 72 degrees C
 PCR cycles: 27
 extension: 6 minutes at 72 degrees C
 Template: 30ng genomic DNA
 Primer: each 1.5 pmole
 dNTPs: each 200 uM
 Taq Polymerase: 0.3 units
 Total Vol: 10 ul

Protocol:

Buffer:

MgCl₂: 1.5mM
 KCl: 50mM
 Tris: 10mM
 pH: 8.3

FEATURES

source

Location/Qualifiers
 1..555
 /organism="Homo sapiens"

STS

primer_bind
 75..317

primer_bind
 complement(298..317)

COUNT 106 a 128 c 101 g 182 t 38 others

IN

Query Match 4.3%; Score 25; DB 4; Length 555;
 Best Local Similarity 85.7%; Pred. No. 1.50e-07;
 Matches 30; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 207 tcttcctctctctctctctctctctctctctc 241

||||| ||||||| ||||||| ||||||| |||||||

Cp 89 TCTTCACTTCTCTCTCTCTCTCTCTCTCTCTCTC 55

RESULT

LOCUS

DEFINITION TgSTzy20h10.r1 Tgrh Tachyzoite cDNA Toxoplasma gondii cDNA clone
 tgy20h10.r1 5'.

ACCESSION N60626

NID g1206777

KEYWORDS EST.

SOURCE Toxoplasma gondii.

ORGANISM Toxoplasma gondii.

Eukaryotae; Mitochondrial eukaryotes; Alveolata; Apicomplexa;

Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.

1 (bases 1 to 307)

Ajioka, J.A., Aslett, M.A., Dietrich, N., Dubuque, T., Hillier, L.,

Kucaba, T., Marra, M., Sibley, L.D., Wan, K.L. and Waterston, R.H.

WashU-Merck Toxoplasma EST Project

Unpublished (1996)

Contact: Marra M

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: toxo@wustl.edu

Clones can be obtained from Genome Systems Inc. (genome@mo.net);

Library can be obtained from Jim Ajioka (jwa@mo.net);

Seq primer: T3

High quality sequence stop: 285.

FEATURES

source

Location/Qualifiers
 1..307
 /organism="Toxoplasma gondii"

/strain="RH"

/note="Vector: Lambda ZAP; Site_1: EcoRI; Site_2: XhoI;

Toxoplasma RH strain tachyzoites were grown in human

foreskin fibroblast cultures in vitro. The library was

constructed by K.L. Wan, Cambridge University. cDNAs were

synthesized from polyA RNAs by oligo d(T) priming and

directionally cloned into the EcoRI to XhoI sites of the

Lambda ZapII vector using the ZAP-cDNA synthesis kit

(Stratagene). WARNING: the library contains a small

(Stratagene).

percentage of cDNAs derived from the human host cells."
 /clone="tgy20h10.r1"

/clone_lib="Tgrh Tachyzoite cDNA"

/lab_host="XLI-Blue MRF"

<1..>307

BASE COUNT 84 a 59 c 93 g 58 t 3 others

ORIGIN

Query Match

Best Local Similarity 4.1%; Score 24; DB 17; Length 307;

Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 122 gaagaagagagagagagagagagagagagag 155

||||| ||||||| ||||||| ||||||| |||||||

QY 55 GAAGAAGAGGTGGAGGAGGAGGAGGAGGTGAAG 88

RESULT

ID

TG626

AC N60626;

NI g1206777

DT 29-FEB-1996 (Rel. 47, Created)

DT 26-JUN-1997 (Rel. 52, Last updated, Version 3)

DE TgSTzy20h10.r1 Tgrh Tachyzoite cDNA Toxoplasma gondii cDNA clone

DE tgy20h10.r1 5'.

KW EST.

OS Toxoplasma gondii

OC Eukaryotae; Mitochondrial eukaryotes; Alveolata; Apicomplexa;

OC Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.

RN [1]

RP 1-307

RA Ajioka J.A., Aslett M.A., Dietrich N., Dubuque T., Hillier L.,

RA Kucaba T., Marra M., Sibley L.D., Wan K.L., Waterston R.H.;

RT "WashU-Merck Toxoplasma EST Project";

RL Unpublished.

CC Contact: Marra M WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC toxo@wustl.edu Clones can be obtained from Genome Systems

CC Inc. (genome@mo.net); library can be obtained from Jim Ajioka

CC (jwa@mo.net); Seq primer: T3 High quality sequence stop:

CC 285.

CC Key

Location/Qualifiers

1..307

/organism="Toxoplasma gondii"

/strain="RH"

/note="Vector: Lambda ZAP; Site_1: EcoRI; Site_2: XhoI;

Toxoplasma RH strain tachyzoites were grown in human

foreskin fibroblast cultures in vitro. The library was

constructed by K.L. Wan, Cambridge University. cDNAs were

synthesized from polyA RNAs by oligo d(T) priming and

directionally cloned into the EcoRI to XhoI sites of the

Lambda ZapII vector using the ZAP-cDNA synthesis kit

(Stratagene). WARNING: the library contains a small

percentage of cDNAs derived from the human host cells."

/clone="tgy20h10.r1"

/clone_lib="Tgrh Tachyzoite cDNA"

/lab_host="XLI-Blue MRF"

<1..>307

SEQUENCE 307 BP; 84 A; 59 C; 93 G; 68 T; 3 other;

Query Match

Best Local Similarity 4.1%; Score 24; DB 92; Length 307;

Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 122 gaagaagagagagagagagagagagagagag 155

||||| ||||||| ||||||| ||||||| |||||||

QY 55 GAAGAAGAGGTGGAGGAGGAGGAGGAGGTGAAG 88

RESULT

LOCUS

12 Hs2682D9

387 bp DNA

STS

28-NOV-1994

Denaturation:	94 degrees C for 15 seconds
Annealing:	58 degrees C for 23 seconds
Polymerization:	72 degrees C for 30 seconds
PCR Cycles:	30
Thermal Cycler:	Perkin Elmer 9600
Protocol:	
Template:	25 ng
Primer:	each 1 uM
dNTPs:	each 200 uM
Taq Polymerase:	0.05 units/ul
Total Vol:	10 ul
Buffer:	
MgCl2:	2.5 mM
KCl:	50 mM
Tris-HCl:	20 mM
pH:	8.3
Chromosome 14.	
Location/Qualifiers	
1..400	
/organism="Homo sapiens"	
180..382	
/map="14"	
180..200	
/map="14"	
complement(361..382)	
/map="14"	
BASE COUNT	112 a 62 c 121 g 80 t 25 others
ORIGIN	
Query Match	4.1%; Score 24; DB 4; Length 400;
Best Local Similarity	92.9%; Pred. No. 2.54e-06;
Matches	26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db	113 aagaaggaggaggaggaggaggagg 140
QY	56 AAGAAGGAGGTGGAGGAGGAGAAGG 83
RESULT	14
LOCUS	G09443 429 bp DNA STS 14-AUG-1995
DEFINITION	human STS CHLC.CCT1.P10053 clone CCT1.
ACCESSION	G09443
NID	G941292
KEYWORDS	STS sequence; primer; sequence tagged site.
SOURCE	human vector-pJCPI host-E.coli dut-tung+ (DH10B) Marker Selected genomic DNA prepared from XY individual of French nationality.
ORGANISM	Homo sapiens Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 429) Murray,J., Sheffield,V, Weber,J.L., Duyk,G. and Buetow,K.H. Cooperative Human Linkage Center Unpublished (1995) Synonyms: CCT1, CHLC.CCT1.P10052 Contact: Dr. Jeffrey C. Murray UofI The University of Iowa Department of Pediatrics, Iowa City, IA 52242, USA Tel: (319) 356-3508 Fax: (319) 356-3347 Email: jeff-murray@uiowa.edu
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
Primer A:	TGCTTCACATTGAGGAGACC
Primer B:	GTTCCTTATGCTGGGATTT
STS size:	117
PCR Profile:	denature: 30 seconds at 94 degrees C annealing: 75 seconds at 55 degrees C

WPAELH (TM)

Release 2.1D John F. Collins, Blocomputing Research Unit.
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MPSICH DN n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Feb-19 10:11:56 1998; MasPar time 156.07 Seconds
1046.228 Million cell updates/sec
No output not generated.

Title: >US-08-910-733-12
Description: (1-579) from US08910733.seq
Perfect Score: 579
N.A. Sequence: 1 CAGAGGACCTCTGTCCTA.....TCCAGGAGGACGAGTAGTAC 579
Comp: GTCTTCTGGAGCAGCAGAT.....AGGTCTCTGCTCATCATG

Scoring table: TABLE default

Nmatch STD : Dbase 0; Query 0

Searched: 397346 seqs, 141010104 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: EST-C

1:EST197 2:EST198 3:EST199 4:EST200 5:EST201 6:EST202

7:EST203 8:EST204 9:EST205 10:EST206 11:EST207 12:EST208

13:EST209 14:EST210 15:EST211 16:EST212 17:EST213

18:EST214 19:EST215 20:EST216 21:EST217 22:EST218

23:EST219 24:EST220 25:EST221 26:EST222 27:EST223

28:EST224 29:EST225 30:EST226 31:EST227 32:EST228

33:EST229 34:EST230 35:EST231 36:EST232 37:EST233

38:EST234 39:EST235 40:EST236 41:EST237 42:EST238

43:EST239 44:EST240 45:EST241 46:EST242 47:EST243

48:EST244 49:EST245 50:EST246 51:EST247 52:EST248

53:EST249 54:EST250 55:EST251 56:EST252 57:EST253

58:EST254 59:EST255 60:EST256 61:EST257 62:EST258

63:EST259 64:EST260 65:EST261 66:EST262 67:EST263

68:EST264 69:EST265 70:EST266 71:EST267 72:EST268

73:EST269 74:EST270 75:EST271 76:EST272 77:EST273

78:EST274 79:EST275 80:EST276 81:EST277 82:EST278

83:EST279 84:EST280 85:EST281 86:EST282 87:EST283

88:EST284 89:EST285 90:EST286 91:EST287 92:EST288

93:EST289 94:EST290 95:EST291 96:EST292 97:EST293

98:EST294

EST-D

99:EST295 100:EST296 101:EST297 102:EST298 103:EST299

104:EST300 105:EST301 106:EST302 107:EST303 108:EST304

109:EST305 110:EST306 111:EST307 112:EST308 113:EST309

114:EST310 115:EST311 116:EST312 117:EST313 118:EST314

119:EST315

Statistics: Mean 10.606; Variance 2.226; scale 4.764

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	244	42.1	349	60	AA381142	EST94184 Activated T-	0.00e+00
2	43	7.4	301	37	AA327613	EST30995 Cornea I Hom	7.15e-33
3	27	4.7	513	67	AA214768	vc72b10.s1 Knowles So	1.09e-09
4	25	4.3	258	111	RICS13404A	Rice cdNA, partial se	3.47e-07
5	25	4.3	447	18	AA110445	ml61d06.r1 Stratagene	5.54e-06
6	24	4.1	232	73	AA344012	EST49871 Gall bladder	5.54e-06
7	24	4.1	534	12	AA241374	mw23b05.r1 Soares mou	5.54e-06
8	24	4.1	542	67	AA413832	vc72b10.s1 Knowles So	5.54e-06
9	24	4.1	588	88	AA054719	zk68d04.s1 Soares pre	5.54e-06
10	23	4.0	203	110	RICS10830A	Rice cdNA, partial se	8.15e-05
11	23	4.0	226	109	RICG11126A	Rice cdNA, partial se	8.15e-05
12	23	4.0	242	111	RICS4040A	Rice cdNA, partial se	8.15e-05
13	23	4.0	270	110	RICS0735A	Rice cdNA, partial se	8.15e-05
14	23	4.0	272	112	AA45033	vg57g05.r1 Beddington	8.15e-05
15	23	4.0	275	111	RICS14303A	Rice cdNA, partial se	8.15e-05
16	23	4.0	286	110	RICS10413A	Rice cdNA, partial se	8.15e-05
17	23	4.0	289	111	RICS4688A	Rice cdNA, partial se	8.15e-05
18	23	4.0	296	109	RICG10912A	Rice cdNA, partial se	8.15e-05
19	23	4.0	303	4	AA214819	mu73h08.r1 Stratagene	8.15e-05
20	23	4.0	308	111	RICS2342A	Rice cdNA, partial se	8.15e-05
21	23	4.0	309	110	RICR0440A	Rice cdNA, partial se	8.15e-05
22	23	4.0	323	109	RICS11195A	Rice cdNA, partial se	8.15e-05
23	23	4.0	330	110	RICG1213A	Rice cdNA, partial se	8.15e-05
24	23	4.0	331	109	RICG1058A	Rice cdNA, partial se	8.15e-05
25	23	4.0	345	111	RICS1545A	Rice cdNA, partial se	8.15e-05
26	23	4.0	350	46	AA269991	va55e07.r1 Soares mou	8.15e-05
27	23	4.0	354	81	AA411362	zv29g09.r1 Soares ova	8.15e-05
28	23	4.0	367	11	AA238683	mx82h11.r1 Soares mou	8.15e-05
29	23	4.0	385	111	RICS14660A	Rice cdNA, partial se	8.15e-05
30	23	4.0	395	7	AA227161	zr20b10.s1 Stratagene	8.15e-05
31	23	4.0	402	111	RICS4292A	Rice cdNA, partial se	8.15e-05
32	23	4.0	402	111	RICS1848A	Rice cdNA, partial se	8.15e-05
33	23	4.0	406	6	AA221237	mw11b02.r1 Soares mou	8.15e-05
34	23	4.0	410	111	RICS2872A	Rice cdNA, partial se	8.15e-05
35	23	4.0	410	111	RICS1750A	Rice cdNA, partial se	8.15e-05
36	23	4.0	419	32	AA316084	EST187957 HCC cell li	8.15e-05
37	23	4.0	421	47	AA272945	va39g06.r1 Soares mou	8.15e-05
38	23	4.0	428	11	AA236110	zs05e11.r1 Soares NDH	8.15e-05
39	23	4.0	457	117	C19433	Rice cdNA, partial se	8.15e-05
40	23	4.0	459	117	C20070	Rice cdNA, partial se	8.15e-05
41	23	4.0	459	117	C20080	Rice cdNA, partial se	8.15e-05
42	23	4.0	502	46	AA268866	va59g07.r1 Soares mou	8.15e-05
43	23	4.0	780	64	AA391050	LD09995.5prime LD Dro	8.15e-05
44	22	3.8	556	101	AA439252	LD13764.5prime LD Dro	1.09e-03
45	22	3.8	583	79	AA401892	zt44d09.s1 Soares ova	1.09e-03

ALIGNMENTS

1
RESULT AA381142 349 bp mRNA EST 21-APR-1997
LOCUS EST94184 Activated T-cells I Homo sapiens cdNA 5' end similar to
DEFINITION Interleukin 1 receptor antagonist (GB:X52015).
ACCESSION AA381142
NID g2033462
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
REFERENCE 1 (bases 1 to 349)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man,Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

Other ESTs: EST94183 THC166385

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tadb/hgi.html>)

Seq primer: M13 Reverse.

FEATURES

source

1..349

/organism="Homo sapiens"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

/clone_lib="Activated T-cells I"

/cell_type="T-lymphocyte"

/dev_stage="adult"

<1...>349

98 a 78 c 78 g 87 t 8 others

BASE COUNT

ORIGIN

Query Match 42.1%; Score 244; DB 60; Length 349;

Best Local Similarity 94.7%; Pred. No. 0.00e+00;

Matches 266; Conservative 0; Mismatches 12; Indels 3; Gaps 3;

Db 69 gagacgatctgccgaccctctggagaaatccagcaagatgcagcattcagaatctgg 128

QY 106 GAGACGATCTGCCGACCTCTGGGAGAAATCCAGCAGATGCAGCCTTCAGATCTGG 165

129 gatgttaacagagacatttatctgagggaacaccacactagttgctggtgatacttgcac 188

QY 166 GATGTTAACAGAGACCTTCTATCTGAGGAACACCACTAGTGTCTGGATCTTGCAA 225

Db 189 ggaccaaattgcaatttagaagaaatagatgtgtaccattgagcctcatgctctg 248

QY 226 GGACCAATGTCAATTAGAAAGAAAGATAGTGGTACCATGAGCCCTGCTCTG 285

Db 249 tcttgggnatccatnagggaagatgtgcctgttctgttgcagctcttggtagagac 308

QY 286 TTCTTGGGAATCCATGAGGGAAGATGTGCCTGTCTGTCAAGTCT-GGTGATGAGAC 344

Db 309 cagaatcagctttnnaggnttaacattagacattag 349

QY 345 CAGACTCCAGT-GGAGGCAGTT-AACATCAGTACGCTGAG 383

RESULT 2

LOCUS AA327613 301 bp mRNA EST 20-APR-1997

DEFINITION EST30995 Cornea I Homo sapiens cDNA 5' end similar to Interleukin 1 receptor antagonist (GB:M55646).

ACCESSION AA327613

NID G1979878

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea.

1 (bases 1 to 301)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brannon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitch, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

TITLE

JOURNAL

MEDLINE

COMMENT

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

Other ESTs: THC168458

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tadb/hgi.html>)

Seq primer: M13 Reverse.

FEATURES

source

1..301

/organism="Homo sapiens"

/note="Organ: cornea; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

/clone_lib="Cornea I"

/dev_stage="adult"

<1...>301

53 a 99 c 75 g 62 t 2 others

BASE COUNT

ORIGIN

Query Match 7.4%; Score 43; DB 37; Length 301;

Best Local Similarity 100.0%; Pred. No. 7.15e-33;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 cgtcatgtccaaatcttacttcagaggagagtagtac 43

QY 537 CGTCATGTCTCCAAATCTTACTTCCAGGAGGAGTAGTAC 579

RESULT 3

LOCUS AA414768 513 bp mRNA EST 08-MAY-1997

DEFINITION vc72b10.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone

ACCESSION AA414768

NID G2074945

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 513)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,


```

Tsukuba Ibaraki
Japan 305
Phone: 0298-38-7441
Fax : 0298-38-7468.

FEATURES
    source
        1..258
        /organism="Oryza sativa"
        /strain="Nipponbare"
        /dev_stage="Green shoot (8 days old)"
        35 a      81 c  97 g  40 t      5 Others

BASE COUNT
ORIGIN

Query Match          4.3%; Score 25; DB 111; Length 258;
Best Local Similarity 77.3%; Pred. No. 3.47e-07;
Matches 34; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 2 tttncttgactgtgttcgagagagagagagagagagaag 45
    ||| ||||| ||| ||| ||||| ||||| ||||| |||||
QY 39 TTTAGTGACTTGTATGAGAGAGGAGGTGGAGGAGGAGAAG 82

RESULT 5
LOCUS AAL10445 447 bp mRNA EST 03-FEB-1997
DEFINITION ml61d06.r1 Stratagene mouse testis (#937308) Mus musculus cDNA
ACCESSION G110445
NID Q1662213
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; mitochondriol eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.

REFERENCE
1 (bases 1 to 447)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
        Geisell,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
        Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
        Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
        Waterston,R.
        The WashU-HMMI Mouse EST Project
        Unpublished (1996)

TITLE The WashU-HMMI Mouse EST Project
JOURNAL
COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine#
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:310339
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 404.
        Location/Qualifiers
            1..447
            /organism="Mus musculus"
            /strain="Inbred CD-1"
            /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
            /XhoI; Cloned unidirectionally. Primer: Oligo dt. Average
            insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
            sequence: 5' GAATTCGCACGAG 3' -3' adaptor sequence: 5'
            CTCGAGTGTGTGTGTGTGTGTGTGT 3"
            /clone="516491"
            /clone_lib="Stratagene mouse testis (#937308)"
            /sex="males"
            /dev_stage="10-12 week old"
            /lab_host="SOLR (kanamycin resistant)"
            <1..>447

170 a      83 c  154 g  40 t

mRNA
BASE COUNT
ORIGIN

```


[illegible]

[illegible]

[illegible]

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```

Title: >US-08-910-733-13
Description: (1-180) from US08910733.pep
Perfect Score: 1298
Sequence: 1 MALADLYEEGGGGGEGEDN.....

```

Searched: 111726 seqs, 13889129 residues

Database: a-zeneseq30

Statistics: Mean 31.298; Variance 121.057; scale 0.259

SUMMARIES

Report No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1298	100.0	180	17	R91361	Intracellular IL-1 re	2,79e-127
2	1140	87.8	159	3	R15362	Variant IL-1 cytokine	6,13e-110
3	1140	87.8	177	17	R98251	Interleukin-1 recepto	6,13e-110
4	1140	87.8	177	14	R75784	Human IL-1 receptor a	6,13e-110
5	1140	87.8	177	3	R144000	IRAP.	6,13e-110
6	1137	87.6	177	17	R98253	Interleukin-1 recepto	1,31e-109
7	1137	87.6	177	18	R99262	Human interleukin-1 r	1,31e-109
8	1134	87.4	177	17	R98252	Interleukin-1 recepto	2,78e-109
9	1134	87.4	177	18	R99263	Human interleukin-1 r	2,78e-109
10	1131	87.1	159	13	R73642	iCtL-1ra.	5,94e-109
11	1130	87.1	165	3	P93816	Sequence encoded by b	7,64e-109
12	1131	87.1	177	18	R99261	Human interleukin-1 r	5,94e-109
13	1131	87.1	177	13	R73641	IL-1ra.	5,94e-109
14	1130	87.1	177	7	R35485	IL-11-2A fragment.	7,64e-109
15	1130	87.1	177	3	P96159	Sequence of interleuk	7,64e-109
16	1100	84.7	152	7	R35486	IL-1 inhibitor (IL-1i	1,48e-105
17	1095	84.4	152	5	R27958	Native IL-1ra polypep	5,20e-105
18	1086	82.1	177	7	R35489	IL-1 inhibitor (IL-1i	7,77e-102
19	996	76.7	177	3	P91515	Sequence of interleuk	4,48e-94
20	419	32.3	90	7	R35484	IL-1i fragment.	4,77e-32

RESULT 2
 ID R15262 standard; Protein; 159 AA.
 AC R15262;
 DT 13-FEB-1992 (first entry)
 DE Variant IL-1 cytokine inhibitor.
 KW Intracellular; Interleukin-1; cancer; immunosuppressive.
 OS Homo sapiens.
 PN W09117249-A.
 PD 14-NOV-1991.
 PR 01-MAY-1990; US-517276.
 PA (CETU) CETUS CORP.
 PA (UYNC) UNIV NORTH CAROLINA.
 PI Haskill JS, Martin G, Ralph P.
 DR WPI; 91-353770/48.
 DR N-PSDB; Q14843.
 PT New Interleukin-1 antagonists - used to diagnose conditions
 mediated by IL-1 and to treat and prevent sepsis and cancer
 Claim 7; Fig 2; 42pp; English.
 CC The amino acid sequence is that of an intracellular protein having
 cytokine inhibitory activity, it is a variant interleukin-1 (IL-1)
 cytokine inhibitor. The DNA encoding the inhibitor can be used to
 determine the number of copies of the inhibitor gene present per
 cell in various types of cancers and so measure the degree of over-
 amplification. The inhibitor can be administered to patients at high
 risk of developing sepsis or who have already developed it. It may
 also have immunosuppressive effects against rheumatoid arthritis.
 CC also have immunosuppressive effects against rheumatoid arthritis.
 SQ Sequence 159 AA;
 Query Match 87.8%; Score 1140; DB 3; Length 159;
 Best Local Similarity 100.0%; Pred. NO. 6.13e-110;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 4 eticrpsgrksskmqafriwvndqktfyrlnnqlvagylogpnvnleekidvvpiephal 63
 QY 25 ETICRPSGRKSSKMQAFRIWDVNDQKTFLRNQVLVAGYLOGPNVNLEKIDVVP1EPHAL 84
 Db 64 flgihgkmcscvksqgdetrlqlleavnitdlseknkqdkrfafirsdgpttsfesaac 123
 QY 85 FLIGHGKMCSCVKSQGDTRQLQLEAVNITDLSENKQDKRFAFIRSDSGPTTSFESAC 144
 Db 124 pgwflctameadqpsvsltnmpdegvmvtfkfyqede 159
 QY 145 PGWFLCTAMEADQPSVSLTNMPDEGVMTKFFQDE 180
 RESULT 3
 ID R98251 standard; Protein; 177 AA.
 AC R98251;
 DT 23-SEP-1996 (first entry)
 DE Interleukin-1 receptor antagonist.
 KW Drug delivery; Escherichia coli; Bacillus subtilis;
 KW Lactobacillus; interleukin-1 receptor antagonist; IL-1ra;
 KW septic shock; therapy.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label- Sig.peptide
 FT Protein 26..177
 FT /label- Mat.protein
 PN W09611277-A1.
 PD 18-APR-1996.
 PR 05-OCT-1994; E03921.
 PA (DOMP-) DOMPE SPA.
 PI Boraschi D, Bossu P, Macchia G, Maurizi G, Porzio S;
 PI Ruggero P, Tagliabue A;
 DR WPI; 96-209858/21.
 DR N-PSDB; T30157.
 PT Engineered microorganisms expressing therapeutic proteins - useful
 PT as therapeutic delivery systems for the treatment of disease.
 PS Disclosure; Fig 4; 77pp; English.

CC Human interleukin-1 receptor antagonist (IL-1ra) (R98251) is
 CC structurally similar to IL-1 and binds with high affinity to the
 CC IL-1 receptor but does not activate target cells. It has potential
 CC as a therapeutic agent for the treatment of inflammatory and
 CC matrix-destruction diseases e.g. septic shock. cDNA (see also
 CC T30157) coding for IL-1ra or for IL-1ra mutants (R98252-53) can be
 CC inserted into a vector to allow expression in Bacillus subtilis
 CC transformants. In vivo administration of these transformants
 CC results in detectable plasma levels of IL-1ra, demonstrating trans-
 CC mucosal absorption of a recombinant therapeutic protein produced by
 CC a microbial host.
 SQ Sequence 177 AA;
 Query Match 87.8%; Score 1140; DB 17; Length 177;
 Best Local Similarity 100.0%; Pred. NO. 6.13e-110;
 Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 22 eticrpsgrksskmqafriwvndqktfyrlnnqlvagylogpnvnleekidvvpiephal 81
 QY 25 ETICRPSGRKSSKMQAFRIWDVNDQKTFLRNQVLVAGYLOGPNVNLEKIDVVP1EPHAL 84
 Db 82 flgihgkmcscvksqgdetrlqlleavnitdlseknkqdkrfafirsdgpttsfesaac 141
 QY 85 FLIGHGKMCSCVKSQGDTRQLQLEAVNITDLSENKQDKRFAFIRSDSGPTTSFESAC 144
 Db 142 pgwflctameadqpsvsltnmpdegvmvtfkfyqede 177
 QY 145 PGWFLCTAMEADQPSVSLTNMPDEGVMTKFFQDE 180
 RESULT 4
 ID R75784 standard; Protein; 177 AA.
 AC R75784;
 DT 02-FEB-1996 (first entry)
 DE Human IL-1 receptor antagonist.
 KW IL-1 receptor antagonist; IL-1; IL-3; IL-4; IL-10; human;
 KW tumour necrosis factor alpha; moloney murine leukaemia virus;
 KW rheumatoid arthritis; systemic lupus erythematosus; osteoporosis;
 KW osteogenesis imperfecta; Sjorgen's syndrome; systemic sclerosis;
 KW polymyositis-dermatomyositis; vasculitis syndrome; psoriatic arthritis;
 KW ankylosing spondylitis; Paget's disease; inflammatory bowel disease;
 KW synovocyte; keratinocyte; chondrocyte; polymorphonuclear leukocyte.
 OS Homo sapiens.
 PN W09516353-A1.
 PD 22-JUN-1995.
 PR 12-DEC-1994; U14337.
 PR 14-DEC-1993; US-167642.
 PA (UYPI-) UNIV PITTSBURGH.
 PI Evans CH, Robbins PD;
 DR WPI; 95-231292/30.
 DR N-PSDB; 090813.
 PT Systemic gene therapy of connective tissue diseases, e.g. rheumatoid
 PT arthritis - using viral vectors to deliver nucleotide sequences
 PT encoding therapeutic peptides/proteins esp. IL-1 receptor antagonist
 PT protein
 PS Example 6; Page 44; 68pp; English.
 CC This sequence represents interleukin-1 receptor antagonist protein
 CC (IRAP). This protein is a product of activated macrophages. The protein
 CC is also produced in synovocytes, keratinocytes, chondrocytes and
 CC polymorphonuclear leukocytes. IRAP is a weak inhibitor of the biological
 CC activities of IL-1. IRAP production is increased by a variety of
 CC cytokines and other stimuli including IL-1, IL-3, IL-4, IL-10 and tumour
 CC necrosis factor alpha (TNF-alpha). The cDNA encoding this sequence can
 CC be introduced into a moloney murine leukaemia virus (MoMuLV) vector. This
 CC vector can then be used in methods of treating a variety of autoimmune
 CC and non-autoimmune diseases involving pathogenesis of connective tissue
 CC which promotes inflammation, cytokine mediation and tissue destruction.
 CC These conditions include rheumatoid arthritis, systemic lupus
 CC erythematosus, osteogenesis imperfecta, osteoporosis, Sjorgen's syndrome,
 CC polymyositis-dermatomyositis, systemic sclerosis, vasculitis syndromes,
 CC juvenile rheumatoid arthritis, ankylosing spondylitis, psoriatic
 CC arthritis, Paget's disease and inflammatory bowel disease. The advantage
 CC of using a vector containing IRAP is that it can be used to provide

CC multiple delivery sites, and prolonged activity of the protein within the
CC patient, which are problems encountered with current methods.
SQ Sequence 177 AA;

Query Match 87.8%; Score 1140; DB 14; Length 177;
Best Local Similarity 100.0%; Pred. No. 6.13e-110; Mismatches 0; Indels 0; Gaps 0;
Matches 156; Conservative 0;

Db 22 eticrpsgrksskmqafriwvngkftfyrnnqlvlgpnvnleekidvvpiephal 81

QY 25 ETICRPSGRKSSKMQAFRIWVNGKFTFYRNNQLVAGLQGNVLEEKIDVVPPIEPHAL 84

Db 82 flighgkmcslscvsgdetrqlqleavnidlsenrkqdkrfafirsdspttsfesaac 141

QY 85 FLIGHGKMCCLSCVSGDETRQLQLEAVNITDLSNRKQDKRFAFIRSDSGPTTSFESAAC 144

Db 142 pgwfcltameadqpsvltmnpdgvmtkfyfqed 177

QY 145 PGWFCLTAMEADQPSVLTNMPDEGVMTKFFQDE 180

IT R14400 standard; Protein; 177 AA.
AC R14400;
DT 17-FEB-1992 (first entry)

DE IRAP.

OS Sclavo peptide; MIRAP; interleukin; receptor; inhibitor.

OS Homo sapiens.

PH Key Location/Qualifiers

FT Peptide 1..15

FT /label= sig_peptide

FT Protein 26..177

FT /label= mat_protein

FT Modified site 109

FT /label= N-glycosylation_site

PN W09117184-A.

PD 14-NOV-1991.

PF 03-APR-1991; U02127.

PR 27-APR-1990; US-515468.

PA (URJO) UPJOHN CO.

PI Carter DB;

DR WPI; 91-353724/48.

DR N-PSDB; Q14693.

PT New DNA molecules are modified Interleukin-1 inhibitors -

PT comprising an IL-1 receptor antagonist protein and a Sclavo

PT protein, useful for treating arthritis

PS Disclosure: Page 25, 29pp; English.

CC In order to construct improved Interleukin-1 Receptor Agonist

CC Protein (IRAP), manipulations are performed on the IRAP gene to

CC insert oligonucleotides (Q14690-92) that encode a Sclavo peptide

CC into the appropriate region of the IRAP gene.

CC See also Q14690-4.

SQ Sequence 177 AA;

Query Match 87.8%; Score 1140; DB 3; Length 177;
Best Local Similarity 100.0%; Pred. No. 6.13e-110;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 22 eticrpsgrksskmqafriwvngkftfyrnnqlvlgpnvnleekidvvpiephal 81

QY 25 ETICRPSGRKSSKMQAFRIWVNGKFTFYRNNQLVAGLQGNVLEEKIDVVPPIEPHAL 84

Db 82 flighgkmcslscvsgdetrqlqleavnidlsenrkqdkrfafirsdspttsfesaac 141

QY 85 FLIGHGKMCCLSCVSGDETRQLQLEAVNITDLSNRKQDKRFAFIRSDSGPTTSFESAAC 144

Db 142 pgwfcltameadqpsvltmnpdgvmtkfyfqed 177

QY 145 PGWFCLTAMEADQPSVLTNMPDEGVMTKFFQDE 180

RESULT 6

ID R98253 standard; Protein; 177 AA.

AC R98253;

DT 23-SEP-1996 (first entry)

DE Interleukin-1 receptor antagonist T109A mutant.

KW Drug delivery; Escherichia coli; Bacillus subtilis;

KW Lactobacillus; Interleukin-1 receptor antagonist; IL-1ra;

KW septic shock; therapy.

OS Synthetic.

PH Key Location/Qualifiers

FT Peptide 1..25

FT /label= sig_peptide

FT Protein 26..177

FT /label= Mat_protein

FT /note= "T109A mutant refers to position 109

FT of the mature protein (134 of the

FT full-length sequence)"

PN W09611277-A1.

PD 18-APR-1996.

PF 04-OCT-1995; E03921.

PR 05-OCT-1994; IT-MI2025.

PA (DOMP-) DOMPE SPA.

PI Boraschi D, Bossu P, Macchia G, Maurizi G, Porzio S;

PI Ruggiero P, Tagliabue A;

DR WPI; 96-209858/21.

DR N-PSDB; T30159.

DR Engineered microorganisms expressing therapeutic proteins - useful

DR as therapeutic delivery systems for the treatment of disease.

PT Example 2; Fig 4; 77pp; English.

PS The T109A mutant (R98253) of human interleukin-1 receptor antagonist

CC (IL-1ra) (see also R98251) has an alanine residue substituting

CC for threonine at position 109 of the mature protein. The mutant

CC retains the activity of native IL-1ra, binding with high affinity to

CC the IL-1 receptor, and has potential as a therapeutic agent for the

CC treatment of inflammatory and matrix-destruction diseases e.g. septic

CC shock. cDNA (T30159) coding for the mutant can be inserted into a

CC vector to allow expression in Bacillus subtilis transformants. In

CC vivo administration of these transformants results in detectable

CC plasma levels of IL-1ra, demonstrating trans-mucosal absorption of a

CC recombinant therapeutic protein produced by a microbial host.

SQ Sequence 177 AA;

Query Match 87.6%; Score 1137; DB 17; Length 177;
Best Local Similarity 99.4%; Pred. No. 1.31e-109;
Matches 155; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 22 eticrpsgrksskmqafriwvngkftfyrnnqlvlgpnvnleekidvvpiephal 81

QY 25 ETICRPSGRKSSKMQAFRIWVNGKFTFYRNNQLVAGLQGNVLEEKIDVVPPIEPHAL 84

Db 82 flighgkmcslscvsgdetrqlqleavnidlsenrkqdkrfafirsdspttsfesaac 141

QY 85 FLIGHGKMCCLSCVSGDETRQLQLEAVNITDLSNRKQDKRFAFIRSDSGPTTSFESAAC 144

Db 142 pgwfcltameadqpsvltmnpdgvmtkfyfqed 177

QY 145 PGWFCLTAMEADQPSVLTNMPDEGVMTKFFQDE 180

RESULT 7

ID R99262 standard; Protein; 177 AA.

AC R99262;

DT 06-NOV-1996 (first entry)

DE Human interleukin-1 receptor antagonist mutant, M1RA-2.

KW Interleukin-1 receptor; antagonist; IL-1; inflammatory disease;

KW rheumatoid arthritis; allergy; graft rejection; autoimmune disease;

OS Synthetic.

PH Key Location/Qualifiers

FT Peptide 1..25

FT /label= sig_peptide

FT Protein 26..177

FT /label= mat_protein

FT Misc.difference 134

FT /label= substitution

FT /note= "Thr to Ala substitution i.e. Thr appears at
 FT this position in the wild-type protein"
 PN W09609323-Al.
 PD 28-MAR-1996.
 PF 20-SEP-1995; E03708.
 PR 21-SEP-1994; IT-MI1916.
 PA (DOMP-) DOMPE SPA.
 PI Boraschi D, Bossu P, Frascotti G, Frigerio F, Grandi G;
 PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;
 DR WPI; 96-188402/19.
 DR N-PSDB; T35255.
 PT Interleukin-1 receptor antagonist mutants - have enhanced
 PT inhibitory activity, useful for the treatment of rheumatoid
 PT arthritis, allergies, graft rejection, etc.
 PS Claim 1; Page -; 41pp; English.
 CC R99261-R99263 are mutant versions of a human interleukin-1 (IL-1)
 CC receptor antagonist protein, MILRA-3, MILRA-2 and MILRA-1 respectively.
 CC They contain at least one of the following two substitutions: Asn to
 CC Arg at position 91 of the mature protein or Thr to Ala at position
 CC 109 of the mature protein. The IL-1 receptor antagonist mutants have
 CC an improved capacity for interaction with IL-1 receptor type I (largely
 CC responsible for cell activation in response to IL-1). The mutant
 CC proteins can be used in the prepn. of drugs capable of antagonising the
 CC inflammatory, neurological, endocrinological, haematological, metabolic,
 CC catabolic and immunostimulant effects associated with IL-1, and in
 CC particular for the treatment of acute or chronic inflammatory
 CC pathologies e.g. rheumatoid arthritis.
 SQ Sequence 177 AA;

Query Match 87.68; Score 1137; DB 18; Length 177;
 Best Local Similarity 99.4%; Pred. No. 1.31e-109;
 Matches 155; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 22 eticrpsgrksskmqafriwvngkftfyrlnnqlvagylqgpnvnleekidvvpiephal 81
 QY 25 ETICRPSGRKSSKMQAFRIWDVNGKFTFYLNNQLVAGLQGNVNLEEKIDVVPPIEPHAL 84
 Db 82 flighgkmcscvsgdetrqlqleavnitdlsenrkqdkrfafirsdsqgtsfesaac 141
 QY 85 FLIGHGKMCSCVSGDETRQLQLEAVNITDLSENRKQDKRFARIRSDSGPTTSFESAC 144
 Db 142 pgwflctameadqpsvltmnpdegvmvkfyqede 177
 QY 145 PGWFLCTAMEADQPSVLTNMPDEGVMTKFFQDE 180

RESULT 8
 ID R98252 standard; Protein; 177 AA.
 AC R98252;
 DE 23-SEP-1996 (first entry)
 DE Interleukin-1 receptor antagonist C91R mutant.
 KW Drug delivery; Escherichia coli; Bacillus subtilis;
 KW Lactobacillus; interleukin-1 receptor antagonist; IL-1ra;
 KW septic shock; therapy.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= Sig_peptide
 FT Protein 26..177
 FT /label= Mat_protein
 FT Misc_difference 116
 FT /label= substitution
 FT /note= "Asn to Arg substitution i.e. Asn appears at
 FT this position in the wild-type protein"
 PN W09611277-Al.
 PD 18-APR-1996.
 PF 04-OCT-1995; E03921.
 PR 05-OCT-1994; IT-MI2025.
 PA (DOMP-) DOMPE SPA.
 PI Boraschi D, Bossu P, Macchia G, Maurizi G, Porzio S;
 PI Ruggiero P, Tagliabue A;
 DR WPI; 96-209858/21.
 DR N-PSDB; T30158.
 PT Engineered microorganisms expressing therapeutic proteins - useful

PT as therapeutic delivery systems for the treatment of disease.
 PS Example 2; Fig 4; 77pp; English.
 CC The C91R mutant (R98252) of human interleukin-1 receptor antagonist
 CC (IL-1ra) (see also R98251) has an arginine residue substituting
 CC for cysteine at position 91 of the mature protein. The mutant
 CC retains the activity of native IL-1ra, binding with high affinity to
 CC the IL-1 receptor, and has potential as a therapeutic agent for the
 CC treatment of inflammatory and matrix-destruction diseases e.g. septic
 CC shock. cDNA (T30158) coding for the mutant can be inserted into a
 CC vector to allow expression in Bacillus subtilis transformants. In
 CC vivo administration of these transformants results in detectable
 CC plasma levels of IL-1ra, demonstrating trans-mucosal absorption of a
 CC recombinant therapeutic protein produced by a microbial host.
 SQ Sequence 177 AA;

Query Match 87.4%; Score 1134; DB 17; Length 177;
 Best Local Similarity 99.4%; Pred. No. 2.78e-109;
 Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 22 eticrpsgrksskmqafriwvngkftfyrlnnqlvagylqgpnvnleekidvvpiephal 81
 QY 25 ETICRPSGRKSSKMQAFRIWDVNGKFTFYLNNQLVAGLQGNVNLEEKIDVVPPIEPHAL 84
 Db 82 flighgkmcscvsgdetrqlqleavnitdlsenrkqdkrfafirsdsqgtsfesaac 141
 QY 85 FLIGHGKMCSCVSGDETRQLQLEAVNITDLSENRKQDKRFARIRSDSGPTTSFESAC 144
 Db 142 pgwflctameadqpsvltmnpdegvmvkfyqede 177
 QY 145 PGWFLCTAMEADQPSVLTNMPDEGVMTKFFQDE 180

RESULT 9
 ID R9263 standard; Protein; 177 AA.
 AC R9263;
 DE 06-NOV-1996 (first entry)
 DE Human interleukin-1 receptor antagonist mutant, MILRA-1.
 KW Interleukin-1 receptor; antagonist; IL-1; inflammatory disease;
 KW rheumatoid arthritis; allergy; graft rejection; autoimmune disease;
 KW recombinant; vector.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= sig_peptide
 FT Protein 26..177
 FT /label= mat_protein
 FT Misc_difference 116
 FT /label= substitution
 FT /note= "Asn to Arg substitution i.e. Asn appears at
 FT this position in the wild-type protein"
 PN W09609323-Al.
 PD 28-MAR-1996.
 PF 20-SEP-1995; E03708.
 PR 21-SEP-1994; IT-MI1916.
 PA (DOMP-) DOMPE SPA.
 PI Boraschi D, Bossu P, Frascotti G, Frigerio F, Grandi G;
 PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;
 DR WPI; 96-188402/19.
 DR N-PSDB; T35256.
 PT Interleukin-1 receptor antagonist mutants - have enhanced
 PT inhibitory activity, useful for the treatment of rheumatoid
 PT arthritis, allergies, graft rejection, etc.
 PS Claim 1; Page -; 41pp; English.
 CC R99261-R99263 are mutant versions of a human interleukin-1 (IL-1)
 CC receptor antagonist protein, MILRA-3, MILRA-2 and MILRA-1 respectively.
 CC They contain at least one of the following two substitutions: Asn to
 CC Arg at position 91 of the mature protein or Thr to Ala at position
 CC 109 of the mature protein. The IL-1 receptor antagonist mutants have
 CC an improved capacity for interaction with IL-1 receptor type I (largely
 CC responsible for cell activation in response to IL-1). The mutant
 CC proteins can be used in the prepn. of drugs capable of antagonising the
 CC inflammatory, neurological, endocrinological, haematological, metabolic,
 CC catabolic and immunostimulant effects associated with IL-1, and in

CC particular for the treatment of acute or chronic inflammatory
 CC Pathologies e.g. rheumatoid arthritis.
 SQ Sequence 177 AA;

Query Match 87.4%; Score 1134; DB 18; Length 177;
 Best Local Similarity 99.4%; Pred. No. 2,78e-109;
 Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 22 eticrpsgrkskmafrivdngktfyrlnnqlvagylogpnvnleekidvvpiephal 81
 QY 25 ETICRPSGRKSSKMAFRIVDNGKTFYLRNQLVAGYLOGPNVNLEEKIDVVP
 Db 82 flghgkmclscvsgdetrilqlavnitdlserrkqdkrfafirsdgpttsfesaac 141
 QY 85 FLGHGKMCLSCVSGDETRILQLEAVNITDLSERNKQDKRFAFIRSDSGPTTSFESAA 144

Db 142 pgwfclctameadqpsvsltnmpdegvmvtkfyfqed 177
 QY 145 PGWFCLCTAMEADQPSVSLTNMPDEGVMTKFFQDE 180

Query Match 87.1%; Score 1131; DB 13; Length 159;
 Best Local Similarity 98.7%; Pred. No. 5,94e-109;
 Matches 154; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 4 eticrpsgrkskmafrivdngktfyrlnnqlvagylogpnvnleekidvvpiephal 63
 QY 25 ETICRPSGRKSSKMAFRIVDNGKTFYLRNQLVAGYLOGPNVNLEEKIDVVP
 Db 64 flghgkmclscvsgdetrilqlavnitdlserrkqdkrfafirsdgpttsfesaac 123
 QY 85 FLGHGKMCLSCVSGDETRILQLEAVNITDLSERNKQDKRFAFIRSDSGPTTSFESAA 144

Db 124 pgwfclctameadqpsvsltnmpdegvmvtkfyfqed 159
 QY 145 PGWFCLCTAMEADQPSVSLTNMPDEGVMTKFFQDE 180

RESULT 11
 ID P93616 standard; Protein; 165 AA.
 AC P93616;

Query Match 87.1%; Score 1130; DB 3; Length 165;
 Best Local Similarity 99.4%; Pred. No. 7,64e-109;
 Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 10 eticrpsgrkskmafrivdngktfyrlnnqlvagylogpnvnleekidvvpiephal 69
 QY 25 ETICRPSGRKSSKMAFRIVDNGKTFYLRNQLVAGYLOGPNVNLEEKIDVVP
 Db 70 flghgkmclscvsgdetrilqlavnitdlserrkqdkrfafirsdgpttsfesaac 129
 QY 85 FLGHGKMCLSCVSGDETRILQLEAVNITDLSERNKQDKRFAFIRSDSGPTTSFESAA 144

Db 130 pgwfclctameadqpsvsltnmpdegvmvtkfyfqed 165
 QY 145 PGWFCLCTAMEADQPSVSLTNMPDEGVMTKFFQDE 180

RESULT 12
 ID R99261 standard; Protein; 177 AA.
 AC R99261;
 DT 06-NOV-1996 (first entry)
 DE Human interleukin-1 receptor antagonist mutant, MILRA-3.
 KW Interleukin-1 receptor; antagonist; IL-1; inflammatory disease;
 KW rheumatoid arthritis; allergy; graft rejection; autoimmune disease;
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= sig_peptide
 FT Protein 26..177
 FT /label= mat_protein
 FT /label= difference 116
 FT /label= substitution
 FT /note= "Asn to Arg substitution i.e. Asn appears at
 FT this position in the wild-type protein"
 FT Misc_difference 134
 FT /label= substitution
 FT /note= "Thr to Ala substitution i.e. Thr appears at
 FT this position in the wild-type protein"
 FN WO9609323-A1.
 PD 28-MAR-1996.
 PF 20-SEP-1995; E03708.
 PR 21-SEP-1994; IT-MI1916.

DT 14-MAR-1992 (first entry)
 DE Sequence encoded by bps 61-600 of interleukin-1 inhibitor
 DE (IL-1i) gene.
 KW Interleukin-1 inhibitor; inflammation therapy;
 KW immunosuppressive agent; inflamed joint.
 OS Homo sapiens.
 PN EP-343684-A.
 PD 29-NOV-1989.
 PR 26-MAY-1989; 109540.
 PR 27-MAY-1988; US-199915.
 PR 31-AUG-1988; US-238171.
 PR 31-AUG-1988; US-238173.
 PR 23-SEP-1988; US-248521.
 PR 03-NOV-1988; US-266531.
 PA (SYNE-) SYNERGEN INC.
 PI Hannum CH, Eisenberg SP, Thompson RC, Arend WP, Joslin FG,
 PI Sommer A;
 DR WPI; 89-349765/48.
 DR N-PSDB; N92441.
 PT Purified interleukin-1 inhibitor - used as an immuno-suppressing
 PT agent or to prevent tissue destruction at sites of inflammation
 PS Claim 18; Page 28; 53pp; English.
 CC The inventors specifically claim recombinant DNA molecule Grl0-IL1i-
 CC 2A; and the interleukin-1 inhibitors IL-1i-X, IL-1i-alpha and IL-1i-
 CC beta. The preferred component is cDNA or a genomic polynucleotide
 CC sequence. It includes bases 99-557 of Grl0-IL1i-2A (see N92441-
 CC N92443). Also claimed is a purified interleukin-1 inhibitor (IL-1i),
 CC which is active against 1 or more than 1 of IL-1alpha and IL-1beta.
 SQ Sequence 165 AA;

Query Match 87.1%; Score 1130; DB 3; Length 165;
 Best Local Similarity 99.4%; Pred. No. 7,64e-109;
 Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 10 eticrpsgrkskmafrivdngktfyrlnnqlvagylogpnvnleekidvvpiephal 69
 QY 25 ETICRPSGRKSSKMAFRIVDNGKTFYLRNQLVAGYLOGPNVNLEEKIDVVP
 Db 70 flghgkmclscvsgdetrilqlavnitdlserrkqdkrfafirsdgpttsfesaac 129
 QY 85 FLGHGKMCLSCVSGDETRILQLEAVNITDLSERNKQDKRFAFIRSDSGPTTSFESAA 144

Db 130 pgwfclctameadqpsvsltnmpdegvmvtkfyfqed 165
 QY 145 PGWFCLCTAMEADQPSVSLTNMPDEGVMTKFFQDE 180

RESULT 12
 ID R99261 standard; Protein; 177 AA.
 AC R99261;
 DT 06-NOV-1996 (first entry)
 DE Human interleukin-1 receptor antagonist mutant, MILRA-3.
 KW Interleukin-1 receptor; antagonist; IL-1; inflammatory disease;
 KW rheumatoid arthritis; allergy; graft rejection; autoimmune disease;
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= sig_peptide
 FT Protein 26..177
 FT /label= mat_protein
 FT /label= difference 116
 FT /label= substitution
 FT /note= "Asn to Arg substitution i.e. Asn appears at
 FT this position in the wild-type protein"
 FT Misc_difference 134
 FT /label= substitution
 FT /note= "Thr to Ala substitution i.e. Thr appears at
 FT this position in the wild-type protein"
 FN WO9609323-A1.
 PD 28-MAR-1996.
 PF 20-SEP-1995; E03708.
 PR 21-SEP-1994; IT-MI1916.

(DOMP-) DOMPE SPA.
 PA Boraschi D, Bossu P, Frascotti G, Frigerio F, Grandi G;
 PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;
 DR WPI; 96-188402/19.
 DR N-PSDB; T13177.
 PT Interleukin-1 receptor antagonist mutants - have enhanced
 PT inhibitory activity, useful for the treatment of rheumatoid
 PT arthritis, allergies, graft rejection, etc.
 PS Claim 1; Page 4; 41pp; English.
 CC R99261-R99263 are mutant versions of a human interleukin-1 (IL-1)
 CC receptor antagonist protein, IL1RA-3, IL1RA-2 and IL1RA-1 respectively.
 CC They contain at least one of the following two substitutions: Asn to
 CC Arg at position 91 of the mature protein or Thr to Ala at position
 CC 109 of the mature protein. The IL-1 receptor antagonist mutants have
 CC an improved capacity for interaction with IL-1 receptor type I (largely
 CC responsible for cell activation in response to IL-1). The mutant
 CC proteins can be used in the prep. of drugs capable of antagonising the
 CC inflammatory, neurological, endocrinological, haematological, metabolic,
 CC catabolic and immunostimulant effects associated with IL-1, and in
 CC particular for the treatment of acute or chronic inflammatory
 CC pathologies e.g. rheumatoid arthritis.
 SQ Sequence 177 AA;
 Query Match 87.1%; Score 1131; DB 18; Length 177;
 Best Local Similarity 98.7%; Pred. No. 5.94e-109;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 22 eticrpsgrksskmaqfrlwdvngktfvlrnqnlvagylggnvnleekidvvpiephal 81
 QY 25 ETICRPSGRKSSKMAQFRlWDVNGKTFVLRNQLVAGYLGGNVNLEEKIDVVPiEPHAL 84
 Db 82 flghgkmcslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqgpttsfesaac 141
 QY 85 FLGIHGKMCslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqgpttsfESAAC 144
 Db 142 pgwflctameadqpsvsltnmpdegvmvtkfyqede 177
 QY 145 PGWFLCTAMEADQPVSltNMPDEGVMTKfYQEDE 180
 RESULT 13
 ID R73641 standard; Protein; 177 AA.
 AC R73641;
 DT 28-NOV-1995 (first entry)
 DE IL-1ra.
 KW Interleukin-1; receptor antagonist; ovulation prevention; embryo;
 KW implantation; contraceptive.
 KW Homo sapiens.
 DR W09510298-A.
 PF 12-OCT-1994; U11588.
 PR 12-OCT-1993; US-136077.
 PA (POLA/) POLAN M L.
 PA (POLA/) POLAN M.
 PA (SIMO/) SIMON C.
 PI Polan ML, Simon C, Polan M;
 DR WPI; 95-169961/22.
 DR N-PSDB; Q89792.
 PT Method of contraception using interleukin-1 receptor antagonist -
 PT prevents ovulation and implantation of embryo, also contraceptive
 PT device comprising the antagonist
 PS Disclosure; Fig 6; 59pp; English.
 CC The sequence is that of the polypeptide IL-1ra, an interleukin-1
 CC receptor antagonist. This polypeptide can be used in a
 CC composition (claimed) to prevent ovulation and implantation of an
 CC embryo in a mammalian uterus. The IL-1 receptor antagonist is
 CC useful in contraceptive compans. It is also useful after the
 CC fertilisation event and provide an alternative to known means of
 CC terminating pregnancy post-fertilisation.
 CC See also R73642.
 SQ Sequence 177 AA;
 Query Match 87.1%; Score 1131; DB 13; Length 177;
 Best Local Similarity 98.7%; Pred. No. 5.94e-109;
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Db 22 eticrpsgrksskmaqfrlwdvngktfvlrnqnlvagylggnvnleekidvvpiephal 81
 QY 25 ETICRPSGRKSSKMAQFRlWDVNGKTFVLRNQLVAGYLGGNVNLEEKIDVVPiEPHAL 84
 Db 82 flghgkmcslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqgpttsfesaac 141
 QY 85 FLGIHGKMCslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqgpttsfESAAC 144
 Db 142 pgwflctameadqpsvsltnmpdegvmvtkfyqede 177
 QY 145 PGWFLCTAMEADQPVSltNMPDEGVMTKfYQEDE 180

Best Local Similarity 99.4%; Pred. No. 5.94e-109;
 Matches 155; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 22 eticrpsgrksskmaqfrlwdvngktfvlrnqnlvagylggnvnleekidvvpiephal 81
 QY 25 ETICRPSGRKSSKMAQFRlWDVNGKTFVLRNQLVAGYLGGNVNLEEKIDVVPiEPHAL 84
 Db 82 flghgkmcslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqgpttsfesaac 141
 QY 85 FLGIHGKMCslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqgpttsfESAAC 144
 Db 142 pgwflctameadqpsvsltnmpdegvmvtkfyqede 177
 QY 145 PGWFLCTAMEADQPVSltNMPDEGVMTKfYQEDE 180
 RESULT 14
 ID R35485 standard; Protein; 177 AA.
 AC R35485;
 DT 26-AUG-1993 (first entry)
 DE IL-1i-2A fragment.
 KW Interleukin-1 inhibitor; immunosuppressive; inflammation; cytokine;
 KW collagenase.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..25
 FT /note= "part of N-terminal signal sequence;
 FT claim 12, page 28"
 FT Protein 26
 FT /label= IL-1i
 FT /modified_site 109
 FT /note= "N residue that is part of a
 FT consensus N-glycosylation site"
 FT Misc_difference 26
 FT /note= "P residue; but no P has been
 FT detected at this position (the N-terminus)
 FT of form X of IL-1i; this residue may be
 FT modified in the mature protein"
 PN EP-541920-A.
 PD 19-MAY-1993.
 PF 26-MAY-1989; 109540.
 PR 27-MAY-1988; US-199915.
 PR 31-AUG-1988; US-238713.
 PR 23-SEP-1988; US-248521.
 PR 03-NOV-1988; US-266531.
 PA (SYND) SYNERGEN INC.
 PI Arend WP, Eisenberg SP, Hannum CH, Joslin FG, Sommer A;
 PI Thompson RC;
 DR WPI; 93-160536/20.
 DR N-PSDB; Q40753.
 PT New interleukin-1 inhibiting peptide and DNA - useful as
 PT immunosuppressant for treating auto-immune and other immune
 PT disorders
 PS Disclosure; Fig 14; 55pp; English.
 CC A plaque, GT10-IL-1i-2A, was isolated from a GT10 library, using
 CC the probes given in Q40757-61.
 CC IL-1i is useful as an immunosuppressive agent. When applied
 CC locally it can be used to prevent tissue destruction in an inflamed
 CC joint and other inflammation sites. This protective effect may be
 CC improved if IL-1i is given with collagenase inhibitors.
 CC Sequence 177 AA;
 SQ
 Query Match 87.1%; Score 1130; DB 7; Length 177;
 Best Local Similarity 99.4%; Pred. No. 7.64e-109;
 Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 22 eticrpsgrksskmaqfrlwdvngktfvlrnqnlvagylggnvnleekidvvpiephal 81
 QY 25 ETICRPSGRKSSKMAQFRlWDVNGKTFVLRNQLVAGYLGGNVNLEEKIDVVPiEPHAL 84
 Db 82 flghgkmcslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqgpttsfesaac 141
 QY 85 FLGIHGKMCslcvsksgdetrqlqleavnitdlsernkqdkrfafirsdsqgpttsfESAAC 144

Db 142 pgwflctameadqpsltnmpdegvmvtkfyfgede 177
QY 145 PGWFLCTAMEADQPSLTNPDEGMVMTKIFYFQEDE 180

RESULT 15

ID P96159 standard; Protein; 177 AA.
AC P96159;
DT 14-MAR-1992 (first entry)
DE Sequence of interleukin-1 inhibitor (IL-1i) encoded by the
DE protein coding region of lambda GT10-IL1i-2A.
KW Interleukin-1 inhibitor; inflammation therapy;
KW immunosuppressive agent; inflamed joint.
OS Homo sapiens.
PN EP-343684-A.
PD 29-NOV-1989.
PF 26-MAY-1989; 109540.
PR 27-MAY-1988; US-199915.
PR 31-AUG-1988; US-238171.
PR 31-AUG-1988; US-238713.
PR 23-SEP-1988; US-248521.
PR 03-NOV-1988; US-266531.
PA (SYNE-) SYNERGEN INC.
PI Hannum CH, Eisenberg SP, Thompson RC, Arend WP, Joslin FG,
PI Sommer A;
DR WPI; 89-349765/48.
DR N-PSDB; N92443.
PT Purified interleukin-1 inhibitor - used as an immuno-suppressing
PT agent or to prevent tissue destruction at sites of inflammation
PS Disclosure; Fig 14; 53pp; English.
CC The inventors specifically claim recombinant DNA molecule GT10-IL1i-
CC 2A; and the interleukin-1 inhibitors IL-1i-X, IL-1i-alpha and IL-1i-
CC beta. The preferred component is cDNA or a genomic polynucleotide
CC sequence. It includes bases 99-557 of GT10-IL1i-2A (see N92441-
CC N92443). Also claimed is a purified interleukin-1 inhibitor (IL-1i),
CC which is active against 1 or more than 1 of IL-lalpha and IL-lbeta.
SQ Sequence 177 AA;

Query Match 87.1%; Score 1130; DB 3; Length 177;
Best Local Similarity 99.4%; Pred. No. 7.64e-109;
Matches 155; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 22 eticppsgkrskmqafriwdvndqkfylnnqlvagylqgnvnleekidvvpiephal 81
QY 25 ETICRPSGRKSKMQAFRIWDVNQKTFYLRNQLVAGYLGQPNVLEEKIDVVPTEPHAL 84
Db 82 flghgkmcslscvksgetrlqlleavnitdlseknqdkrfafirsdgpttsfesaac 141
QY 85 FLGHGKMKCLSCVKSGDETRLQLEAVNITDLSENKQDKRFARIRSDSGPTTSFSAAC 144
Db 142 pgwflctameadqpsltnmpdegvmvtkfyfgede 177
QY 145 PGWFLCTAMEADQPSLTNPDEGMVMTKIFYFQEDE 180

Search completed: Thu Feb 19 10:09:49 1998
Job time : 30 secs.

M P E R L H

(TM)

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MPsrch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Feb 19 09:59:47 1998; MasPar time 82.65 Seconds
808.366 Million cell updates/sec

Par output not generated.

Title: >US-08-910-733-12
Description: (1-579) from US08910733.seq
Perfect Score: 579
N.A. Sequence: 1 CAGAAGGACCTCTCTGCTTA.....TCCAGGAGGACGAGTAGTAC 579
Comp: GTCTTCTCTGGAGCAGGAT.....AGGTCTCTCTGCTCATCATG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-genes30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 8.641; Variance 5.257; scale 1.644

Pred. No. is the number of results predicted by chance to have a
Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES					% Match		Query		Pred. No.	
Result No.	Score	Match	Length	ID	Description					
1	579	100.0	579	22	T15099	Intracellular IL-1 re	0.00e+00			
2	474	81.9	589	15	Q90813	Human IL-1 receptor	0.00e+00			
3	474	81.9	611	3	Q14843	Variant IL-1 cytokine	0.00e+00			
4	472	81.5	540	3	N92441	Sequence of bps 61-60	0.00e+00			
5	472	81.5	600	7	Q40753	Sequence of bps 61-60	0.00e+00			
6	472	81.5	600	3	N92443	Sequence of GT10-IL1	0.00e+00			
7	469	81.0	532	3	Q14693	IRAP gene.	6.79e-302			
8	468	80.8	531	21	T30157	Interleukin-1 recepto	3.42e-301			
9	467	80.7	557	15	Q89792	IL-1ra gene.	1.72e-300			
10	467	80.7	602	15	Q89793	iCtL-1ra gene.	1.72e-300			
11	466	80.5	531	22	T35255	Human interleukin-1 r	8.64e-300			
12	466	80.5	531	21	T30159	Interleukin-1 recepto	8.64e-300			
13	464	80.1	531	21	T30158	Interleukin-1 recepto	2.19e-298			
14	464	80.1	531	22	T35256	Human interleukin-1 r	2.19e-298			
15	460	79.4	531	22	T13177	Human interleukin-1 r	1.40e-295			

16	456	78.8	456	7	Q40754	IL-1 inhibitor (IL-1i	8.92e-293
17	454	78.4	514	30	T72210	DNA encoding leaderle	2.25e-291
18	454	78.4	514	13	Q83763	Plasmid i5424.	2.25e-291
19	453	78.2	717	30	T72209	DNA encoding interleu	1.13e-290
20	453	78.2	717	13	Q83762	IL1 receptor-antagoni	1.13e-290
21	186	32.1	270	7	Q40752	Lambda GT10-IL-1i-2A,	3.51e-105
22	186	32.1	270	3	N92442	Sequence of part of t	3.51e-105
23	55	9.5	1047	2	Q10572	Human Natriuretic Pep	1.30e-18
24	51	8.8	1047	2	Q10572	Human Natriuretic Pep	1.30e-18
25	43	7.4	91	9	Q51746	Oligonucleotide probe	1.95e-11
26	40	6.9	58	2	Q11920	Sequence encoding fir	1.06e-09
27	39	6.7	204	1	N81164	Base substituted E.co	3.94e-09
28	38	6.6	204	1	N81164	Base substituted E.co	1.45e-08
29	37	6.4	91	9	Q51746	Oligonucleotide probe	5.33e-08
30	34	5.9	114	12	Q70467	Generic DNA sequence	2.47e-06
31	34	5.9	114	12	Q70468	Generic DNA sequence	2.47e-06
32	33	5.7	114	12	Q70471	Generic DNA sequence	8.71e-06
33	32	5.5	114	12	Q70465	Generic DNA sequence	3.03e-05
34	32	5.5	986	1	N82421	Sequence of human per	3.03e-05
35	32	5.5	1497	10	Q58462	IL-1 beta gene.	3.03e-05
36	31	5.4	114	12	Q70469	Generic DNA sequence	1.04e-04
37	31	5.4	178	31	T76405	Human endothelin-1 an	1.04e-04
38	31	5.4	460	2	N60284	Sequence encoding new	1.04e-04
39	31	5.4	1750	1	N80433	Bovine interleukin-1	1.04e-04
40	30	5.2	469	30	T72208	DNA encoding human in	3.53e-04
41	30	5.2	478	13	Q83760	Plasmid pDM15449.	3.53e-04
42	30	5.2	579	2	N60285	Sequence encoding new	3.53e-04
43	30	5.2	702	30	T72205	DNA encoding mature h	3.53e-04
44	30	5.2	702	13	Q83758	Plasmid 16963.	3.53e-04
45	30	5.2	1507	3	N50060	Sequence encoding int	3.53e-04

ALIGNMENTS

RESULT 1

ID T15099 standard; cDNA; 579 BP.

AC T15099;

DT 22-OCT-1996 (first entry)

DE Intracellular IL-1 receptor antagonist type II.

KW Intracellular IL-1 receptor antagonist; icIL-1ra;

KW secreted IL-1 receptor antagonist; sIL-1ra;

KW interleukin; IL-1a; IL-1B; auto-immune disease; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 34..576

FT /tag= a

PN W09612022-A1.

PD 25-APR-1996.

PF 12-OCT-1995; E04023.

PR 13-OCT-1994; IT-MI2097.

PA (ISTF) ARS APPLIED RES SYST HOLDING NV.

PI Colotta F, Mantovani A, Muzio M;

DR WPI; 96-222008/22.

DR P-PSDB; R91361.

PT IL-1 receptor antagonist active against IL-1a and -1B - for

PT treating, preventing or diagnosing auto-immune diseases

PS Claim 5: Page 22-23; 36pp; English.

CC An new IL-1 receptor antagonist includes the sequence given in R91360.

CC The complete icIL-1ra1 is given in T15099. The protein is

CC expressed by DNA similar to that encoding the known receptor

CC inhibitor icIL-1ra, but having a 63 bp insert between the first

CC icIL-1ra specific exon and the internal acceptor site of the first

CC exon of sIL-1ra.

SQ Sequence 579 BP; 157 A; 146 C; 155 G; 121 T;

Query Match 100.0%; Score 579; DB 22; Length 579;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ddb 1 cagaagacacctctctatgagccctcccccctgcttagctgtatgaagaa 60

Qy 1 CAGAAGGACCTCTCTATGAGGCCCTCCCATGCTTGTATGAGAA 60

CC	IL-3, IL-4, IL-10 and tumour necrosis factor alpha (TNF-alpha). This sequence can be introduced into a moloney murine leukemia virus (MOMLV) vector. This vector can then be used in methods of treating a variety of autoimmune and non-autoimmune diseases involving pathogenesis of connective tissue which promotes inflammation, cytokine mediation and tissue destruction. These conditions include rheumatoid arthritis, systemic lupus erythematosus, osteogenesis imperfecta, osteoporosis, Sjorgen's syndrome, polymyositis-dermatomyositis, systemic sclerosis, vasculitis syndromes, juvenile rheumatoid arthritis, ankylosing spondylitis, psoriatic arthritis, Paget's disease and inflammatory bowel disease. The advantage of using a vector containing IRAP is that it can be used to provide multiple delivery sites, and prolonged activity of the protein within the patient, which are problems encountered with current methods.	Seq
Query Match	81.9%; Score 474; DB 15; Length 589;	
Best Local Similarity	100.0%; Pred. No. 0.00e+00;	
Matches	474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Sequence	589 BP; 150 A; 165 C; 141 G; 133 T;	
78	gagacgattctgcgcgaccctctggagaaaaatccagcaagatcgaaagccttcgaattctg	137
106	GAGAGAGATCTGCCGACCTCTGGGAGAAATCCAGAGATGCAAGCTTCAGAAATCTGG	165
138	gatgttaaccagaagaccctctatctgatggagcaaccaactagttgctgatacttgc	197
166	GATGTTAACCAGAGACCTTCTATCTGAGGAACAACCAACTAGTTGCTGGATACTTCAA	225
198	gaccaaattgtaatttagaagaaaagatagtgtgtacccattgagcctcatgctctg	257
226	GGACCAAAATGTCAATTTAGAAGAAAGATAGATGTGGTACCATTTGAGCCTCATGCTCTG	285
258	tcttggaaatccatggaggaaagatgtgccttcctctgtctcaagtcgtggtgatgagacc	317
286	TTCTTGGGAATCCATGGAGGAAGATGTGCTCTGCTGTCAAGCTGTGTGATGAGACC	345
318	agactccagctggagcgagttaaacatcactgacctgagcgagagacaagaagcaggacaag	377
346	AGACTCCAGCTGGAGGCAGTTAATCATCACTGACCTGAGCGGAGACACAAGCAGGACAAG	405
378	cgcttcgcttoatcgcgtctcagcagctggtgccccaccaccagttttagtctgcgcctgc	437
406	CGCTTGGCCTTCATCCGCTCAGACAGTGGCCCCACCACCAAGTTTGTAGTCTGCCCTGC	465
438	ccgcttggttcctctcagcagcatggaagctgaaagctgacacgcgcgtcagctccaccaatg	497
466	CCCGTGTGGTTCCTCTGCACAGCGATGGAAGCTCACCAGCCGTCACGCCCTCACAATATG	525
498	ctgtcagcagcgctcatggtccacaaattctacttccagagcagcagtagtagtac	551
526	CTGTGAGGAGCGTCATGGTCACCAATTTCTACTTCCAGGAGGACGAGTAGTAGTAC	579
RESULT	3	
ID	Q14843 standard; cDNA; 611 BP.	
AC	Q14843;	
DE	13-FEB-1992 (first entry)	
DT	Variant IL-1 cytokine inhibitor gene.	
DD	Intracellular; interleukin-1; cancer; immunosuppressive; ss.	
DK	Homo sapiens.	
OS	Homo sapiens.	
HF	Key	
FF	Location/Qualifiers	
FT	123..602	
PN	W09117249-A.	
PD	14-NOV-1991.	
PP	10-APR-1991; U02460.	
PR	01-MAY-1990; US-517276.	
PA	(CETU) CETUS CORP.	
PPA	(UUNC-) UNIV NORTH CAROLINA.	
PPI	Haskill JS, Martin G, Ralph P.	
DR	WPI; 91-353770/48.	
DR	P-PSDB; R15262.	
DR	New Interleukin-1 antagonists - used to diagnose conditions	

PT mediated by IL-1 and to treat and prevent sepsis and cancer
PS Claim 1; Fig 2; 42pp; English.
CC The sequence is that encoding an intracellular protein having
CC cytokine inhibitory activity, it is a variant interleukin-1 (IL-1)
CC cytokine inhibitor. The DNA can be used to determine the number
CC of copies of the inhibitor gene present per cell in various types
CC of cancers and so measure the degree of overamplification. The
CC inhibitor can be administered to patients at high risk of
CC developing sepsis or who have already developed it. It may also
CC have immunosuppressive effects against rheumatoid arthritis. See
CC also Q14844.
SQ Sequence 611 BP; 153 A; 166 C; 160 G; 132 T;

Query Match 81.98; Score 474; DB 3; Length 611;
Best Local Similarity 100.08; Pred. No. 0.00e+00;
Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 132 gagaccatctccgaccctctggagaaatccagcaagatgcagccttcagacttg 191
QY 106 GAGACGATCTGCCGACCTCTGGAGAAATCCAGCAAGATGCAAGCCTTCAGAAATCTGG 165
Db 192 gatgttaaccagaagaccttctatctgagaaacacacactagttgctggacttgcaa 251
QY 166 GATGTTAACCAAGACCTTCTATCTGAGGACACACCACTAGTTGCTGGATCTGCAA 225
Db 252 gaacaaatgtcaatttagaagaaagatagtggtgtacccattgagcctcatgctctg 311
QY 226 GGACCAATGTCAATTTAGAAAGAAATAGATGTGTGTACCATTTGAGCCTCATGCTGTG 285
Db 312 tctctgggaatccatgaggaagatgctgtcctgtctgctgctgctgctgctgctg 371
QY 286 TCTCTGGGAATCATGGAGGAGATGTGCTGTCTGTCTCAAGTCTGATGATGAGAC 345
Db 372 agactccagctgagggcagttacatcaactgacctgagcgagagacagagcagacaag 431
QY 346 AGACTCCAGCTGGAGCGAGTTACATCACTGACCTGAGCGGACACAGACAGACAG 405
Db 432 cgcttgccttcacccgctcagacagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 491
QY 406 CGCTTGCCTTCTATCGCTCAGACAGTGGCCGCCACCACTAGTTTGTAGTCTGCGCCTGC 465
Db 492 ccggtgtgtctctgcacagcgatggaagatgacagcccgctcagcctcaccacatg 551
QY 466 CCGGTTGTGTTCTCTGACAGCGATGGAAGCTGACAGCCCGCTCAGCCCTCACCATAATG 525
Db 552 cctgacgaagggctcagtggtccacaaattctacttccagagcagcagtagtac 605
QY 526 CTGACGAGGCGTATGTTGTCACCAATTTCTACTTCCAGGAGGACGAGTAGTAC 579

RESULT 4
ID N92441 standard; DNA; 540 BP.
AC N92441.
DT 14-MAR-1992 (first entry)
DE Sequence of bps 61-600 of interleukin-1 inhibitor (IL-1) gene.
KW Interleukin-1 inhibitor; inflammation therapy;
KW immunosuppressive agent; inflamed joint; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..497
FT /tag= a
FT /codon_start= 3
FT EP-343684-A.
PD 29-NOV-1989.
PF 26-MAY-1989; 109540.
PR 27-MAY-1988; US-199915.
PR 31-AUG-1988; US-238171.
PR 31-AUG-1988; US-238713.
PR 23-SEP-1988; US-248521.
PR 03-NOV-1988; US-266531.
PA (SYNE-) SYNERGEN INC.
PI Hannum CH, Eisenberg SP, Thompson RC, Arend WP, Joslin FG,
PI Sommer A;

DR WPI: 89-349765/48.
DR P-PSDB; P93616.
PT Purified interleukin-1 inhibitor - used as an immuno-suppressing
PT agent or to prevent tissue destruction at sites of inflammation
PS Claim 18; Page 28; 53pp; English.
CC The inventors specifically claim recombinant DNA molecule Gp10-IL1i-
CC 2A; and the interleukin-1 inhibitors IL-1i-X, IL-1i-alpha and IL-1i-
CC beta. The preferred component is cDNA or a genomic polynucleotide
CC sequence. It includes bases 99-557 of Gp10-IL1i-2A (see N92441-
CC N92443). Also claimed is a purified interleukin-1 inhibitor (IL-1i),
CC which is active against 1 or more than 1 of IL-1alpha and IL-1beta.
SQ Sequence 540 BP; 135 A; 150 C; 132 G; 123 T;

Query Match 81.5%; Score 472; DB 3; Length 540;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 473; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 27 gagcagatctccacccctctgggagaaatccagcaagatgcagccttcagacttg 86
QY 106 GAGACGATCTGCCGACCTCTGGAGAAATCCAGCAAGATGCAAGCCTTCAGAAATCTGG 165
Db 87 gatgttaaccagaagaccttctatctgaggaacacacactagttgctggacttgcaa 146
QY 166 GATGTTAACCAAGACCTTCTATCTGAGGACACACCACTAGTTGCTGGATCTGCAA 225
Db 147 ggacaaatgtcaatttagaagaaagatagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 206
QY 226 GGACCAATGTCAATTTAGAAAGAAATAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 285
Db 207 tctctgggaatccatgaggaagatgctgtcctgtcctgtcctgtcctgtcctgtcctgtc 266
QY 286 TCTCTGGGAATCATGGAGGAGATGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 345
Db 267 agactccagctgagggcagttacatcaactgacctgagcgagagacagagcagacaag 326
QY 346 AGACTCCAGCTGGAGCGAGTTACATCACTGACCTGAGCGGACACAGACAGACAG 405
Db 327 cgcttgccttcacccgctcagacagtggt 386
QY 406 CGCTTGCCTTCTATCGCTCAGACAGTGGCCGCCACCACTAGTTTGTAGTCTGCGCCTGC 465
Db 387 ccggtgtgtctctgcacagcgatggaagatgacagcccgctcagcctcaccacatg 446
QY 466 CCGGTTGTGTTCTCTGACAGCGATGGAAGCTGACAGCCCGCTCAGCCCTCACCATAATG 525
Db 447 cctgacgaagggctcagtggtccacaaattctacttccagagcagcagtagtac 500
QY 526 CCGGTTGTGTTCTCTGACAGCGATGGAAGCTGACAGCCCGCTCAGCCCTCACCATAATG 579

RESULT 5
ID Q40753 standard; DNA; 600 BP.
AC Q40753.
DT 26-AUG-1993 (first entry)
DE Gp10-IL-1i-2A fragment.
KW Interleukin-1 inhibitor; immunosuppressive; inflammation; cytokine;
KW collagenase; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 24..557
FT /tag= a
FT sig_peptide 3..98
FT /tag= b
FT /note= "encodes 32 amino acid N-terminal to the
FT amino terminus of the form of IL-1i known as X"
FT sig_peptide 24..98
FT /tag= c
FT /note= "claim 33, page 30"
FT mat_peptide 99..554
FT /tag= c
FT /label= IL-1i
FT misc_feature 349..351
FT /tag= d


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KW Sclavo peptide; IRAP; MIRAP; interleukin; receptor; inhibitor; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT sig_peptide 1..75
FT /*tag= a
FT mat_peptide 76..531
FT /*tag= b
PN WO9117184-A.
PD 14-NOV-1991.
PF 03-APR-1991; U02127.
PR 27-APR-1990; PS-515468.
PA (UPJO ) UPJOHN CO.
PI Carter DB.
PI WPI; 91-353724/48.
DR P-PSDB; R14400.
PT New DNA molecules are modified Interleukin-1 inhibitors -
PT comprising an IL-1 receptor antagonist protein and a sclavo
PT protein, useful for treating arthritis
PS Disclosure: Page 25; 29pp; English.
CC Probe DC-166 (see Q14694) was used to screen a U937 cDNA library.
CC A clone (P5) was isolated and sequenced. The human DNA sequence
CC contains ca. 1782 nucleotides including 5' and 3' nontranslated
CC sequences. The longest ORF begins with nucleotide 53 (1 in this
CC sequence) and extends to nucleotide 584 (532 in this sequence).
CC The sequence is used to produce modified IRAP by addition of
CC Sclavo peptides.
CC See also Q14690-4.
SQ Sequence 532 BP; 138 A; 147 C; 129 G; 118 T;

Query Match 81.0%; Score 469; DB 3; Length 532;
Best Local Similarity 100.0%; Pred. No. 6.79e-302;
Matches 469; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 64 gagacgatcgcgacccctctggagagaaatccagcaagatgcaagccttcagaattctg 123
|||||
QY 106 GAGACGATCTGCGACCCCTCTGGAGAAATCCAGCAAGATGCAAGCCTTCAGAACTGG 165

Db 124 gatgttaaccagaagacccttctatctaggagaaacacaaactagttgctgatactgcaa 183
|||||
QY 166 GATGTTAACCAAGACCTTCTATCTGAGAAACCACTAGTTGCTGGACTACTTGCAA 225

Db 184 gacacaaatgcaatttagaagaaagatagatgtgtgtaacccattgagcctcatgctcg 243
|||||
QY 226 GGACCAATGTCAATTAGAGAAAGATAGATGTGTGCTACCACTGAGCCTCAGTCTCTG 285

Db 244 ttcttggaatccatggaggagatgctgctgctgctgctgctgctgctgctgctgctgctg 303
|||||
QY 286 TTCTTGGGAATCCATGGAGGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 345

Db 304 agactccagctggagcagtttaacatcactgacctgagcgagagacagagagagagagag 363
|||||
QY 346 AGACTCCAGCTGGAGCAGTTAACTACTGACCTGAGCGAGAGAGAGAGAGAGAGAGAGAG 405

Db 364 cgttcgcttccatcgctcagacagatggtggtggtggtggtggtggtggtggtggtggtg 423
|||||
QY 406 CGCTTCGCCTTATCCGCTCAGACAGTGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 465

Db 424 ccggttggttctctgacagcagatggtggtggtggtggtggtggtggtggtggtggtggtg 483
|||||
QY 466 CCGGTGTGTTCTCTGACAGCGATGGAGCTGACAGCGCGCGCGCGCGCGCGCGCGCGCGCG 525

Db 484 cctgacgaaggcgtcatggtcaccacaaattctacttccaggagagcaggt 532
|||||
QY 526 CCTGACGAAGGCGTCATGTCACCAAAATCTACTTCCAGGAGGAGCGAGT 574

RESULT 8
ID T30157 standard; DNA; 531 BP.
AC T30157;
DT 23-SEP-1996 (first entry)
DE Interleukin-1 receptor antagonist cDNA.
KW Drug delivery; Escherichia coli; Bacillus subtilis;
Lactobacillus; interleukin-1 receptor antagonist; IL-1ra;

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KW septic shock; therapy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT sig_peptide 1..75
FT /*tag= a
FT mat_peptide 76..531
FT /*tag= b
PN WO9611277-A1.
PD 18-APR-1996.
PF 04-OCT-1995; E03921.
PR 05-OCT-1994; IT-MI2025.
PA (DOMP-) DOMPE SPA.
PI Boraschi D, Bossu P, Macchia G, Maurizi G, Porzio S;
PI Ruggiero P, Tagliabue A;
DR WPI; 96-209858/21.
PT Engineered microorganisms expressing therapeutic proteins - useful
PT as therapeutic delivery systems for the treatment of disease.
PS Disclosure: Fig 4; 77pp; English.
CC A cDNA clone (T30157) codes for human interleukin-1 receptor
CC antagonist (IL-1ra) (R98251), a protein that is structurally
CC similar to IL-1 and which binds with high affinity to the IL-1
CC receptor but does not activate target cells. It has potential as
CC a therapeutic agent for the treatment of inflammatory and
CC matrix-destruction diseases e.g. septic shock. The cDNA or clones
CC (see also T30158-59) coding for IL-1ra mutants (R98252-53) can be
CC inserted into a vector to allow expression in Bacillus subtilis
CC transformants. In vivo administration of these transformants
CC results in detectable plasma levels of IL-1ra, demonstrating trans-
CC mucosal absorption of a recombinant therapeutic protein produced by
CC a microbial host.
SQ Sequence 531 BP; 138 A; 147 C; 129 G; 117 T;

Query Match 80.8%; Score 468; DB 21; Length 531;
Best Local Similarity 100.0%; Pred. No. 3.42e-301;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 64 gagacgatcgcgacccctctggagagaaatccagcaagatgcaagccttcagaattctg 123
|||||
QY 106 GAGACGATCTGCGACCCCTCTGGAGAAATCCAGCAAGATGCAAGCCTTCAGAACTGG 165

Db 124 gatgttaaccagaagacccttctatctaggagaaacacaaactagttgctgatactgcaa 183
|||||
QY 166 GATGTTAACCAAGACCTTCTATCTGAGAAACCACTAGTTGCTGGACTACTTGCAA 225

Db 184 gacacaaatgcaatttagaagaaagatagatgtgtgtaacccattgagcctcatgctcg 243
|||||
QY 226 GGACCAATGTCAATTAGAGAAAGATAGATGTGTGCTACCACTGAGCCTCAGTCTCTG 285

Db 244 ttcttggaatccatggaggagatgctgctgctgctgctgctgctgctgctgctgctgctg 303
|||||
QY 286 TTCTTGGGAATCCATGGAGGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 345

Db 304 agactccagctggagcagtttaacatcactgacctgagcgagagacagagagagagagag 363
|||||
QY 346 AGACTCCAGCTGGAGCAGTTAACTACTGACCTGAGCGAGAGAGAGAGAGAGAGAGAGAG 405

Db 364 cgttcgcttccatcgctcagacagatggtggtggtggtggtggtggtggtggtggtggtg 423
|||||
QY 406 CGCTTCGCCTTATCCGCTCAGACAGTGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 465

Db 424 ccggttggttctctgacagcagatggtggtggtggtggtggtggtggtggtggtggtggtg 483
|||||
QY 466 CCGGTGTGTTCTCTGACAGCGATGGAGCTGACAGCGCGCGCGCGCGCGCGCGCGCGCG 525

Db 484 cctgacgaaggcgtcatggtcaccacaaattctacttccaggagagcaggt 531
|||||
QY 526 CCTGACGAAGGCGTCATGTCACCAAAATCTACTTCCAGGAGGAGCGAGT 573

RESULT 9
ID Q89792 standard; DNA; 557 BP.
AC Q89792;

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DT	28-NOV-1995 (first entry)	FT	CD5	Key	Location/Qualifiers	FT	CD5	Key	Location/Qualifiers
DE	IL-lra gene.	FT				FT			
DE	Interleukin-1; receptor antagonist; ovulation prevention; embryo;	FT				FT			
KW	implantation; contraceptive; ss.	PN	W09510298-A.			PN	W09510298-A.		
OS	Homo sapiens.	PF	12-OCT-1994; U11588.			PF	12-OCT-1994; U11588.		
FH		PR	12-OCT-1993; US-136077.			PR	12-OCT-1993; US-136077.		
FT		PA	(POLA/) POLAN M L.			PA	(POLA/) POLAN M L.		
FT		PA	(POLA/) POLAN M.			PA	(POLA/) POLAN M.		
FT		PA	(SIMO/) SIMON C.			PA	(SIMO/) SIMON C.		
DR	Polan ML, Simon C, Polan M;	PI	WPI; 95-169961/22.			PI	WPI; 95-169961/22.		
DR	P-PSDB; R73641.	DR	P-PSDB; R73641.			DR	P-PSDB; R73641.		
PT	Method of contraception using interleukin-1 receptor antagonist -	PT	Prevents ovulation and implantation of embryo, also contraceptive			PT	Prevents ovulation and implantation of embryo, also contraceptive		
PS	device comprising the antagonist	PS	Disclosure; Fig 6; 59pp; English.			PS	Disclosure; Fig 6; 59pp; English.		
CC	The sequence is that of the gene encoding IL-lra, an interleukin-1	CC	receptor antagonist. The gene and its product can be used in a			CC	receptor antagonist. The gene and its product can be used in a		
CC	composition (claimed) to prevent ovulation and implantation of an	CC	embryo in a mammalian uterus. The IL-1 receptor antagonist is			CC	composition (claimed) to prevent ovulation and implantation of an		
CC	useful in contraceptive compsns. It is also useful after the	CC	fertilisation event and provide an alternative to known means of			CC	useful in contraceptive compsns. It is also useful after the		
CC	terminating pregnancy post-fertilisation.	CC	See also Q89793.			CC	terminating pregnancy post-fertilisation.		
CC	Sequence 557 BP; 147 A; 153 C; 135 G; 122 T;	CC	Sequence 557 BP; 147 A; 153 C; 135 G; 122 T;			CC	Sequence 557 BP; 147 A; 153 C; 135 G; 122 T;		
Query Match	80.78; Score 467; DB 15; Length 557;	Query Match	80.78; Score 467; DB 15; Length 557;			Query Match	80.78; Score 467; DB 15; Length 557;		
Best Local Similarity	99.6%; Pred. No. 1.72e-300;	Best Local Similarity	99.6%; Pred. No. 1.72e-300;			Best Local Similarity	99.6%; Pred. No. 1.72e-300;		
Matches	469; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Matches	469; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			Matches	469; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
Db	87 gacacgatctgccgaccctctggagaaatccagaagatacaagccctcagaatctgg 146	Db	87 gacacgatctgccgaccctctggagaaatccagaagatacaagccctcagaatctgg 146			Db	87 gacacgatctgccgaccctctggagaaatccagaagatacaagccctcagaatctgg 146		
QY	106 GAGACGATCTGCCGACCCTCTGGGAAATAATCCAGGAATGCAAGCCTTCAGAACTCG 165	QY	106 GAGACGATCTGCCGACCCTCTGGGAAATAATCCAGGAATGCAAGCCTTCAGAACTCG 165			QY	106 GAGACGATCTGCCGACCCTCTGGGAAATAATCCAGGAATGCAAGCCTTCAGAACTCG 165		
Db	147 gatgttaaccagaagaccttctatctgaggaaacaaactagttgctggacttgcaa 206	Db	147 gatgttaaccagaagaccttctatctgaggaaacaaactagttgctggacttgcaa 206			Db	147 gatgttaaccagaagaccttctatctgaggaaacaaactagttgctggacttgcaa 206		
QY	166 GATGTTAAACCAGAAGACCTTCTATCTGAGGAACAACCACTAGTTGCTGATCTGCAA 225	QY	166 GATGTTAAACCAGAAGACCTTCTATCTGAGGAACAACCACTAGTTGCTGATCTGCAA 225			QY	166 GATGTTAAACCAGAAGACCTTCTATCTGAGGAACAACCACTAGTTGCTGATCTGCAA 225		
Db	207 ggaccaaattgcaattagaagaaagatagatgtggtacccattagacctgctctg 266	Db	207 ggaccaaattgcaattagaagaaagatagatgtggtacccattagacctgctctg 266			Db	207 ggaccaaattgcaattagaagaaagatagatgtggtacccattagacctgctctg 266		
QY	226 GGACCAAAATGTCAATTTAGAAGAAAGATAGATGTGTAATGCCCACTTGGAGCTCATGCTCTG 285	QY	226 GGACCAAAATGTCAATTTAGAAGAAAGATAGATGTGTAATGCCCACTTGGAGCTCATGCTCTG 285			QY	226 GGACCAAAATGTCAATTTAGAAGAAAGATAGATGTGTAATGCCCACTTGGAGCTCATGCTCTG 285		
Db	267 ttcttgggaatccatgaggaagatgtgcctctctgtgtcaagtctggtgatgacc 326	Db	267 ttcttgggaatccatgaggaagatgtgcctctctgtgtcaagtctggtgatgacc 326			Db	267 ttcttgggaatccatgaggaagatgtgcctctctgtgtcaagtctggtgatgacc 326		
QY	286 TTCCTGGGAATCCATGGAGGAGATGTGCTCTCTGTGTCAAGTCTGGTGTGATGAGACC 345	QY	286 TTCCTGGGAATCCATGGAGGAGATGTGCTCTCTGTGTCAAGTCTGGTGTGATGAGACC 345			QY	286 TTCCTGGGAATCCATGGAGGAGATGTGCTCTCTGTGTCAAGTCTGGTGTGATGAGACC 345		
Db	327 agactccagctggaggcagttacatcatctgacctgagcgagaacagaagcaggacaag 386	Db	327 agactccagctggaggcagttacatcatctgacctgagcgagaacagaagcaggacaag 386			Db	327 agactccagctggaggcagttacatcatctgacctgagcgagaacagaagcaggacaag 386		
QY	346 AGACTCCAGCTGGAGGAGTTACATCACTGACCTGAGCGAGAAACAGAGAGGACGACAAAG 405	QY	346 AGACTCCAGCTGGAGGAGTTACATCACTGACCTGAGCGAGAAACAGAGAGGACGACAAAG 405			QY	346 AGACTCCAGCTGGAGGAGTTACATCACTGACCTGAGCGAGAAACAGAGAGGACGACAAAG 405		
Db	387 cgcttgccttcatcgctcagacagtggcccaacacacacagtttttagtctcgccgtgc 446	Db	387 cgcttgccttcatcgctcagacagtggcccaacacacacagtttttagtctcgccgtgc 446			Db	387 cgcttgccttcatcgctcagacagtggcccaacacacacagtttttagtctcgccgtgc 446		
QY	406 CGCTTCGCCTTCTATCGCTCAGACATGTGCCCCACCACCACTGTTTTCAGTCTGCCGCTGC 465	QY	406 CGCTTCGCCTTCTATCGCTCAGACATGTGCCCCACCACCACTGTTTTCAGTCTGCCGCTGC 465			QY	406 CGCTTCGCCTTCTATCGCTCAGACATGTGCCCCACCACCACTGTTTTCAGTCTGCCGCTGC 465		
Db	447 cccggttggttcctctgcacagcgatggagctgacagcccgctcagctcaccaatatg 506	Db	447 cccggttggttcctctgcacagcgatggagctgacagcccgctcagctcaccaatatg 506			Db	447 cccggttggttcctctgcacagcgatggagctgacagcccgctcagctcaccaatatg 506		
QY	466 CCGGGTGTGTTCTCTGCAC								

KW Interleukin-1 receptor; antagonist; IL-1; inflammatory disease;
KW rheumatoid arthritis; allergy; graft rejection; autoimmune disease;
OS recombinant; vector; ds.
FH Synthetic.
FT Key
FT CDS Location/Qualifiers
FT 1..531
FT /tag= a
FT /note= "no stop codon"
FT sig_peptide 1..75
FT /tag= b
FT mat_peptide 76..531
FT /tag= c
FT mutation 400..402
FT /tag= d
FT /note= "ACC to GCC substitution, for the preferred
FT Thr to Ala substitution in the mutant IL-1
FT receptor antagonist protein"
PN WO9609323-A1.
PF 20-SEP-1996; E02708
PI 21-SEP-1994; IT-MI1916.
PI (DMP-) DOMPE SPA.
PI Boraschi D, Bossu P, Frascotti G, Frigerio F, Grandi G;
PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;
DR WPI: 96-188402/19.
DR P-PSDB; R99262.
PT Interleukin-1 receptor antagonist mutants - have enhanced
PT inhibitory activity, useful for the treatment of rheumatoid
PT arthritis; allergies, graft rejection, etc.
PS Claim 1; Page -; 41pp; English.
CC T13177, T35255 and T35256 are cDNA sequences encoding mutant
CC versions of a human interleukin-1 (IL-1) receptor antagonist
CC The sequences encode mutants MILRA-3, MILRA-2 and MILRA-1
CC respectively, which contain at least one of the following two
CC substitutions: Asn to Arg at position 91 of the mature protein or
CC Thr to Ala at position 109 of the mature protein. The IL-1 receptor
CC antagonist mutants have an improved capacity for interaction with
CC IL-1 receptor type I (largely responsible for cell activation in
CC response to IL-1). The mutant proteins can be used in the prepn. of
CC drugs capable of antagonising the inflammatory, neurological,
CC endocrinological, haematological, metabolic, catabolic and
CC immunostimulant effects associated with IL-1, and in particular for
CC the treatment of acute or chronic inflammatory pathologies e.g.
CC rheumatoid arthritis.
SQ Sequence 531 BP; 137 A; 147 C; 130 G; 117 T;
Query Match 80.5%; Score 466; DB 22; Length 531;
Best Local Similarity 99.8%; Pred. No. 8.64e-300;
Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
64 gagacgatctgccgaccctctggagagaaatccagcaagatgcaagccttcagaatctgg 123
106 GAGACGATCTGCCGACCCTCTGGAGAGAAATCCAGCAAGATGCAAGCCTTCAGAATCTGG 165
124 gatgttaaccagaagaccttctatctgaggaacaaacactagttgtggtgatacttgcga 183
166 GATGTTAAACAGAGACCTTCTATCTGAGGAACAAACCACTAGTTGCTGGTACTTGC 225
184 ggacaaatgtcaatttagaagaagaatagatgtgtgacccattgagctcgtcgtg 243
226 GGACCAAAATGCAATTTAGAAGAAAGATAGATGTGTGTCAGTGTGTGATGAGACC 285
244 ttcttgggaatccatgaggaagatgtgctgtcctgtgtcaagtgtggtgagacc 303
286 TTCTTGGGAATCCATGAGGAGAGATGTGCTGTCTGTCTCAAGTGTGTGATGAGACC 345
304 agactccagctggaggcagttacatcactgacctgacctgacctgacctgacctgacctg 363
346 AGACTCCAGCTGGAGGAGAGATGTGCTGTCTGTCTCAAGTGTGTGATGAGACC 405
364 cgttcgcttcacgtcctcagacagtggtggtggtggtggtggtggtggtggtggtggtg 423
406 CGTTCGCTTCATCCGCTCAGACAGTGGGCCCCACCACCCAGTTTGTGAGTCTGCGCCTGC 465

Db 424 cccggttggttctctctgcacagcagatggaagctgacccagcccgctcagcctcacaatg 483
Qy 466 CCCGTTGTTCCCTCTGTCACAGCGATGAGCTGACCAAGCCGTCAGCCTACCAATATG 525
Db 484 cctgacaagcgtcatggtccacaaattctacttccagaggagag 531
Qy 526 CTTGACGAAGCGCTGATGGTCCACCAATTTCTACTTCCAGGAGGAGAG 573
RESULT 12
ID T30159 standard; DNA; 531 BP.
AC T30159;
DT 23-SEP-1996 (first entry)
DE Interleukin-1 receptor antagonist mutant T109A cDNA.
KW Drug delivery; Escherichia coli; Bacillus subtilis;
KW Lactobacillus; interleukin-1 receptor antagonist; IL-1ra;
KW septic shock; therapy; ss.
OS Synthetic.
FH Key
FH Location/Qualifiers
FH mutation 400
FH /tag= a
FH /note= "wild-type base a at position 400 is
FH mutated to g, resulting in T109A
FH mutation in the mature IL-1ra protein"
PN WO9611277-A1.
PD 18-APR-1996.
PF 04-OCT-1995; E03921.
PR 05-OCT-1994; IT-MI2025.
PA (DMP-) DOMPE SPA.
PI Boraschi D, Bossu P, Macchia G, Maurizi G, Porzio S;
PI Ruggiero P, Tagliabue A;
DR WPI: 96-209858/21.
DR P-PSDB: R98253
PT Engineered microorganisms expressing therapeutic proteins - useful
PT as therapeutic delivery systems for the treatment of disease.
PS Example 2; Fig 4; 77pp; English.
CC A cDNA clone (T30159) codes for human interleukin-1 receptor
CC antagonist (IL-1ra) mature protein mutant T109A (R98253). It was
CC obtained by site-directed mutagenesis of cDNA (T30157) coding for
CC wild-type IL-1ra (R98251). The mutant retains the activity of
CC IL-1ra. cDNAs coding for wild-type or mutant IL-1ra (see also
CC T30158) can be inserted into a vector to allow expression in Bacillus
CC subtilis transformants. In vivo administration of the transformants
CC results in detectable plasma levels of IL-1ra, demonstrating trans-
CC mucosal absorption of a recombinant therapeutic protein produced by
CC a microbial host.
SQ Sequence 531 BP; 137 A; 147 C; 130 G; 117 T;

Query Match 80.5%; Score 466; DB 21; Length 531;
Best Local Similarity 99.8%; Pred. No. 8.64e-300;
Matches 467; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
64 gagacgatctgccgaccctctggagagaaatccagcaagatgcaagccttcagaatctgg 123
106 GAGACGATCTGCCGACCCTCTGGAGAGAAATCCAGCAAGATGCAAGCCTTCAGAATCTGG 165
124 gatgttaaccagaagaccttctatctgaggaacaaacactagttgtggtgatacttgcga 183
166 GATGTTAAACAGAGACCTTCTATCTGAGGAACAAACCACTAGTTGCTGGTACTTGC 225
184 ggacaaatgtcaatttagaagaagaatagatgtgtgacccattgagctcgtcgtg 243
226 GGACCAAAATGCAATTTAGAAGAAAGATAGATGTGTGTCAGTGTGTGATGAGACC 285
244 ttcttgggaatccatgaggaagatgtgctgtcctgtgtcaagtgtggtgagacc 303
286 TTCTTGGGAATCCATGAGGAGAGATGTGCTGTCTGTCTCAAGTGTGTGATGAGACC 345
304 agactccagctggaggcagttacatcactgacctgacctgacctgacctgacctgacctg 363
346 AGACTCCAGCTGGAGGAGAGATGTGCTGTCTGTCTCAAGTGTGTGATGAGACC 405

364	Db	364	cgccttgcccttcacgcctgcagacagctgcagcccccacgcgcgaagttttagtctgcgcctcgc	423
406	QY	406	CGCTTGGCCCTTCATCGCTCAGACAGTGCCGCCACACACAGTTTGTAGTCTGCGCCTGC	465
424	Db	424	cccgattggttctctgcacacgcagatgaagctgaccagccgctcagctcaccacaatg	483
466	QY	466	CCCGTGTGGTTCTCTGACAGCGATGGAAGCTGACACCGCTCAGCGCTCAGCAATATG	525
484	Db	484	ctctgacgaaggcgctcatggttcaccaaattcttacttccaggaggacgag	531
526	QY	526	CTGACGAGGCGTCATGCTACCAAAATCTACTCCAGGAGGACGAG	573

RESULT 13

ID T30158 standard; DNA: 531 BP.

T30158;

AC 23-SEP-1996 (first entry)

Interleukin-1 receptor antagonist mutant C91R cDNA.

Drug delivery; Escherichia coli; Bacillus subtilis;

Antibacterial; interleukin-1 receptor antagonist; IL-1ra;

septic shock; therapy; ss.

Synthetic.

OS Key Location/Qualifiers

mutation 346..347

FT /*tag= a

FT /note= "wild-type bases aa at positions 346-347

FT are mutated to cg, resulting in C91R

FT mutation in the mature IL-1ra protein"

PN WO9611277-A1.

PD 18-APR-1996. E03921.

PF 04-OCT-1995; E03921.

PI 06-OCT-1994; IT-MI2025.

PPA (DOMP-) DOMPE SPA.

PI BOASCHI D, BOSSI P, Macchia G, Maurizi G, Porzio S;

PI Ruggiero P, Tagliabue A;

PI WP1; 96-209858/21.

PI P-PSDB; R38252.

DR Engineered microorganisms expressing therapeutic proteins - useful

PT as therapeutic delivery systems for the treatment of disease.

PT Example 2; Fig 4; 77pp: English.

CC A cDNA clone (T30158) codes for human interleukin-1 receptor

CC antagonist (IL-1ra) mature protein mutant C91R (R38252). It was

CC obt'd. by site-directed mutagenesis of cDNA (T30157) coding for

CC wild-type IL-1ra (R38251). The C91R mutant retains the activity of

CC IL-1ra. cDNAs coding for wild-type or mutant IL-1ra (see also

CC T30159) can be inserted into a vector to allow expression in Bacillus

CC subtilis transformants. In vivo administration of the transformants

CC results in detectable plasma levels of IL-1ra, demonstrating trans-

CC mucosal absorption of a recombinant therapeutic protein produced by

CC a microbial host.

CC Sequence 531 BP: 136 A; 148 C; 130 G; 117 T;

Query Match 80.1%; Score 464; DB 21; Length 531;

Best Local Similarity 99.6%; Pred. No. 2.19e-298;

Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps

64	Db	64	gagacgactcgcgcaccctctggggaaaaatccagcaagatgcagccttcagaatctgg	123
106	QY	106	GAGACGATCTGCCACCCTCTGGGAGAAAATCCACAGATGCAGCCCTTCAGATCTCG	165
124	Db	124	gatgttaaccagaagacaccttctatctgaggaaaacacctaagtgtcgtggaacttgcga	183
166	QY	166	GATGTAAACCAAGAACCTTCTATCTGAGGAACAACCAACTAGTTGCTGGATCTTGCA	225
184	Db	184	ggaccaaatgtcaatttagaagaaaagatagatggtgtaccattgagcctcagtctg	243
226	QY	226	GGACCAATGTCAATTTAGAGAAAAGATAGATGTGTGTTACCATTTAGCCCTCATGCTG	285
244	Db	244	ttcttgggaatccatggagggaagatgfcctctgctctgtgtcaagtctggtgatgaacc	303
286	QY	286	TTCCTTGGGAATCCATGGAGGGAGATGTGCCCTGCTCTCTGTGTCAAGTCTGGTAGAGACC	345
304	Db	304	agactccagctggagcgagcttaacatcatcactgacgtgagcgagcgacagaacaggacaag	363

QY 106 GAGACGATCTCCGACCCCTCTGGAGAAATCCAGCAAGATGCAAGCCCTTCAGATCTGG 165
Db 124 gatgttaaccagaagacattctatctatctgaggaacaaactagttgctggatacttgcaa 183
QY 166 GATGTTAAACAGAGACCTTCTATCTGAGGAACAACCAACTAGTTGCTGGATCTTGCAA 225
Db 184 ggacaaatgcaattagagaagaaatagatggtgtacccattgagcctcatgctctg 243
QY 226 GGACCAATGCAATTTAGAGAAAGATGATGTGTACCATGAGCCCTCATGCTCTG 285
Db 244 ttctgggaatccatgaggaagatgctgctgctgctgctgctgctgctgctgctgctg 303
QY 286 TTCTGGGAATCAGTGAAGGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 345
Db 304 agactccagctgagggcagcttaacatcactgacgtgagcgcgcgcgcgcgcgcgcgcgc 363
QY 346 AGACTCCAGCTGGAGGAGTAAACATCAGCTGACCTGAGCGAGAACAGAAAGCAGGACAAG 405
Db 364 cgcttcgcttcacccgctcagacagtggtggtggtggtggtggtggtggtggtggtggtg 423
QY 406 CGCTTCGCTTCATCCGCTCAGACAGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 465
Db 424 cctgacgaagc 483
QY 466 CCCGTTGGTTCTCTGTCACAGCGATGGAAGCTGACCGAGCCGCTCAGCCCTCACCCTATG 525
Db 484 cctgacgaagc 531
QY 526 CTTGACGAAGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 573

RESULT 15
ID T13177 standard; cDNA; 531 BP.
AC T13177;
DT 06-NOV-1996 (first entry)
DE Human interleukin-1 receptor antagonist mutant, MILRA-3, cDNA.
KW Interleukin-1 receptor; antagonist; IL-1; inflammatory disease;
KW rheumatoid arthritis; allergy; graft rejection; autoimmune disease;
KW recombinant; vector; ds.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 1..531
FT /*tag= a
FT /*note= "no stop codon"
FT sig_peptide 1..75
FT /*tag= b
FT mat_peptide 76..531
FT /*tag= c
FT mutation 346..348
FT /*tag= d
FT /*note= "AAC to CGC substitution, for the preferred
FT Asn to Arg substitution in the mutant IL-1
FT receptor antagonist protein"
FT mutation 400..402
FT /*tag= e
FT /*note= "ACC to GCC substitution, for the preferred
FT Thr to Ala substitution in the mutant IL-1
FT receptor antagonist protein"
PN WO9609323-A1.
PD 28-MAR-1996.
PF 20-SEP-1995; E03708.
PR 21-SEP-1994; IT-M11916.
PA (DMP-) DOME SPA.
PI Ronaschi, D., Bessu, P., Frascotti G, Frigerio F, Grandi G;
PI Grifantini R, Macchia G, Ruggiero P, Tagliabue A;
DR WPI; 96-188402/19.
DR P-PSDB; R99261.
PT Interleukin-1 receptor antagonist mutants - have enhanced
PT inhibitory activity, useful for the treatment of rheumatoid
PT arthritis, allergies, graft rejection, etc.
PS Claim 1; Page -; 41pp; English.
CC T13177, T35255 and T35256 are cDNA sequences encoding mutant
versions of a human interleukin-1 (IL-1) receptor antagonist protein.

CC The sequences encode mutants MILRA-3, MILRA-2 and MILRA-1
CC respectively, which contain at least one of the following two
CC substitutions: Asn to Arg at position 91 of the mature protein or
CC Thr to Ala at position 109 of the mature protein. The IL-1 receptor
CC antagonist mutants have an improved capacity for interaction with
CC IL-1 receptor type I (largely responsible for cell activation in
CC response to IL-1). The mutant proteins can be used in the prepn. of
CC drugs capable of antagonising the inflammatory, neurological,
CC endocrinological, haematological, metabolic, catabolic and
CC immunostimulant effects associated with IL-1, and in particular for
CC the treatment of acute or chronic inflammatory pathologies e.g.
CC rheumatoid arthritis. 135 A; 147 C; 132 G; 117 T;
SQ Sequence 531 BP; 135 A; 147 C; 132 G; 117 T;
Query Match 79.4%; Score 460; DB 22; Length 531;
Best Local Similarity 99.1%; Pred. No. 1.40e-295;
Matches 464; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Db 64 gagacgatctccgacccctctgggagaaatccagcaagatgcaagccttcagaatctgg 123
QY 106 GAGACGATCTCCGACCCCTCTGGAGAAATCCAGCAAGATGCAAGCCCTTCAGATCTGG 165
Db 124 gatgttaaccagaagacattctatctgaggaacaaactagttgctggatacttgcaa 183
QY 166 GATGTTAAACAGAGACCTTCTATCTGAGGAACAACCAACTAGTTGCTGGATCTTGCAA 225
Db 184 ggacaaatgcaattagagaagaaatagatggtgtacccattgagcctcatgctctg 243
QY 226 GGACCAATGCAATTTAGAGAAAGATAGATGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 285
Db 244 ttctgggaatccatgagggaggaatgctgctgctgctgctgctgctgctgctgctgctg 303
QY 286 TTCTGGGAATCCATGAGGAGGAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 345
Db 304 agactccagctgagggcaggttaacatcactgacgtgagcgcgcgcgcgcgcgcgcgcgc 363
QY 346 AGACTCCAGCTGGAGGCGAGTTAAACATCAGCTGACCTGAGCGAGAACAGAAAGCAGGACAAG 405
Db 364 cgcttcgcttcacccgctcagacagtggtggtggtggtggtggtggtggtggtggtggtg 423
QY 406 CGCTTCGCTTCATCCGCTCAGACAGTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 465
Db 424 cccggttggttcctctgacacgc 483
QY 466 CCCGTTGGTTCTCTGTCACAGCGATGGAAGCTGACCGAGCCGCTCAGCCCTCACCCTATG 525
Db 484 cctgacgaagc 531
QY 526 CTTGACGAAGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 573

Search completed: Thu Feb 19 10:01:31 1998
Job time : 104 secs.

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		ANTAGONIST PROTEIN PRECURSOR (HUMAN);.				
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		NID				
		g1388557				
	KEYWORDS	EST.				

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 ANTAGONIST PROTEIN PRECURSOR (HUMAN);.
 ACCESSION W95637
 NID q1425546
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 442)
 REFERENCE Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultkin,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
 Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT
 Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: mob.REGA+ET
 High quality sequence stop: 314.
 Location/Qualifiers
 1..442
 /organism="Homo sapiens"
 /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
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 TGTACCAATCTGAAGTGGAGCGCGCATCTTTTTTTTTTTTTTTT 3'] ,
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library went through one round of
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 M.Patima Bonaldo. This library was constructed from the
 same fetus as the fetal lung library, Soares fetal lung
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 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
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 Best Local Similarity 97.8%; Pred. No. 0.00e+00;
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 Qy 106 GAGAGCATCTGCCACCCCTCTGGGAGAAAAATCCAGAAATGTCAGAGCTTCGAACTG 165
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 Qy 166 GTATTAACCAAGAGACCTTCTATCTGAGGAACAACCACTAGTTCTGCTGGTACTTGCA 225
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Db 8 cctgtgtcaagtctggtgatgagaccagactccagctgagagcaggttaacatcactgacc 67
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 QY 380 TGAGCGAGACAGAACAGAGCAGCGCTTCGGCTTCATCCGCTCAGACAGTGGCCCA 439
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 QY 440 CCACAGCTTTGAGTCTGCGCCTGCGCGTGTGTTCTCTGTCACAGCGATGGAAGCTG 499
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 Db 188 accagccgtcagctcccaaatatgctgacgaagcggttcacatgggttcacacaaattctt 247
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RESULT 5
 LOCUS R34906 401 bp mRNA EST 02-MAY-1995
 DEFINITION Y959e06.r1 Homo sapiens cDNA clone 36844 5' similar to
 gp:X64532_rnal INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR
 (HUMAN);
 ACCESSION R34906
 NID 9791807
 KEYWORDS EST.
 SOURCE human clone-36844 library-Soares infant brain LNTB vector-lafmid BA
 host-DH10B (ampicillin resistant) primer-M13RP1 Rsite1-Not I
 Rsite2-Hind III Whole brain from a 73 days post natal female. 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5',
 AACTGGAAGATTCGCGCGCAGCAATTTTCTTTTCTTTT 3']; double-stranded
 cDNA was ligated to Hind III adaptors (Pharmacia), digested with
 Not I and directionally cloned into the Not I and Hind III sites of
 the lafmid BA vector. Library went through one round of
 normalization. Library constructed by Bento Soares and M.Fatima
 Bonaldo.
 ORGANISM Homo sapiens
 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 401)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.
 TITLE The WashU-Merck EST Project
 COMMENT GDB: G00-409-345
 Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 High quality sequence stops: 309
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /clone="36844"

BASE COUNT 108 a 93 c 105 g 94 t 1 others
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 Best Local Similarity 97.7%; Pred. No. 0.00e+00;

Matches 253; Conservative 0; Mismatches 0; Indels 6; Gaps 6;
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 QY 106 GAGACGATCTCCGACCTCTGGGAGAAAATCCAGCAAGATGCAAGCTTCAGAATCTGG 165
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 Db 128 gatattaaccagagaccttctctctctgaggaacaaacaaactagttgtggaattcaca 187
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 QY 166 GATGTTAACCAAGAGACCTTCTATCTGAGGAACAACCAACTAGTTGCTGGATCTGCAA 225
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 Db 188 ggacaaatgtcaatttagaagaaaacatagatgtgtaccattgacccatgcctcctg 247
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 QY 226 GGACCAATGTCATTTAGAAAAGATAGATGTTGTTACCATGAGCCCTCATGCTCTG 285
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 Db 248 ttctggggaatccatggaggggaagatgtgctgtctctgttcaagtctgggtgatg 307
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 QY 286 TTCCTGGG-AATCCATGG-AGGG-AAGATGTCCTCTCTCTGT-CAAGTCTGG-TGATG 340
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 Db 308 aggaccagactccagctgg 326
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 QY 341 AG-ACCAGACTCCAGCTGG 358
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RESULT 6
 LOCUS R83257 234 bp mRNA EST 04-AUG-1995
 DEFINITION YP08h09.r1 Homo sapiens cDNA clone 186881 5' similar to
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 (HUMAN);
 ACCESSION R83257
 NID 928134
 KEYWORDS EST.
 SOURCE human clone-186881 library-Soares breast 3NBHst vector-p77T3D
 (Pharmacia) with a modified polylinker host-DH10B (ampicillin
 resistant) primer-M13Rev Rsite1-Not I Rsite2-Eco RI Adult human.
 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
 TGTTCACCAATGAGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
 digested with Not I and cloned into the Not I and Eco RI sites of a
 modified p77T3 vector (Pharmacia). Library went through one round
 of normalization to a Cot = 20. Library constructed by Bento Soares
 and M.Fatima Bonaldo.
 ORGANISM Homo sapiens
 Eucaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Choonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 234)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.
 TITLE The WashU-Merck EST Project
 COMMENT Unpublished (1995)
 Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 High quality sequence stops: 66
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 FEATURES
 source Location/Qualifiers
 1..234
 /organism="Homo sapiens"
 /clone="186881"

BASE COUNT 51 a 75 c 57 g 47 t 4 others
 ORIGIN

Query Match 11.4%; Score 66; DB 51; Length 234;
 Best Local Similarity 94.4%; Pred. No. 6.48e-74;
 Matches 102; Conservative 0; Mismatches 0; Indels 6; Gaps 6;

Db 9 cctgtgtcagtcgtgtagcagaccagacttcagctgagggcaggttaacatcact 68
 |||||
 QY 320 CCGTGTCAAGTCGTGGTGAG -ACCAG-ACT-CCAGCTGGAGG-CAGTTAACATCACT 375
 |||||

Db 69 gaacctgagcggagacagaaagcagacagcgttcgccttcaccc 116
 |||||
 QY 376 GACCTGAGCAGAGACAGACAGACAGCGCTTCGCGCTTCATCC 421
 |||||

RESULT 7
 LOCUS H50548 482 bp mRNA EST 18-SEP-1995
 DEFINITION yp08h09.s1 Homo sapiens cDNA clone 186881 3' similar to
 gb:X64532_rnal INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR
 (HUMAN);.

ACCESSION H50548
 NID 9990389
 KEYWORDS EST.

ORGANISM Homo sapiens
 Eukaryotes; Eumetazoa; Bilateria; Chordata; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 482)
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.
 The WashU-Merck EST Project
 Unpublished (1995)

CONTACT: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 327
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
 Location/Qualifiers
 1..482
 /organism="Homo sapiens"
 /clone="186881"
 <1..>482
 BASE COUNT 101 a 104 c 167 g 103 t 7 others
 ORIGIN

Query Match 5.9%; Score 34; DB 47; Length 482;
 Best Local Similarity 92.1%; Pred. No. 6.16e-20;
 Matches 58; Conservative 0; Mismatches 1; Indels 4; Gaps 4;

Db 385 gtactactgctcctcctggagtagaattngt-accat-acgc-ttcgt-aggcattt 440
 |||||
 Cp 579 GTACTACTGCTCCTCCTGGAGTAGAATTGGTGACCATGACGCCCTTCGTCGACCATATT 520
 |||||
 Db 441 ggt 443

Query Match 11.4%; Score 66; DB 51; Length 234;
 Best Local Similarity 94.4%; Pred. No. 6.48e-74;
 Matches 102; Conservative 0; Mismatches 0; Indels 6; Gaps 6;

Db 9 cctgtgtcagtcgtgtagcagaccagacttcagctgagggcaggttaacatcact 68
 |||||
 QY 320 CCGTGTCAAGTCGTGGTGAG -ACCAG-ACT-CCAGCTGGAGG-CAGTTAACATCACT 375
 |||||

Db 69 gaacctgagcggagacagaaagcagacagcgttcgccttcaccc 116
 |||||
 QY 376 GACCTGAGCAGAGACAGACAGACAGCGCTTCGCGCTTCATCC 421
 |||||

RESULT 8
 LOCUS AA030324 479 bp mRNA EST 21-JAN-1997
 DEFINITION mi08c10.r1 Soares mouse placenta 4NDMP13.5 14.5 Mus musculus cDNA
 clone 459858 5'.

ACCESSION AA030324
 NID 91497479
 KEYWORDS EST.

ORGANISM house mouse.
 Mus musculus
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Mus.
 1 (bases 1 to 479)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)

CONTACT: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:276746
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 467.

FEATURES
 Location/Qualifiers
 1..479
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /note="vector: p7T3D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p7T3 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M.Fatima Bonaldo."
 /clone="459858"
 /clone_lib="Soares mouse placenta 4NDMP13.5 14.5"
 /sex="unknown"
 /dev_stage="adult"
 /lab_host="DH10B"
 <1..>479
 BASE COUNT 148 a 108 c 102 g 121 t
 ORIGIN

Query Match 5.0%; Score 29; DB 188; Length 479;
 Best Local Similarity 78.4%; Pred. No. 1.02e-12;
 Matches 40; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 273 agtggtacaacctctacatttgagctgcagccttcctcgttggttcac 323
 |||||
 QY 430 AGTGGCCCCACACACAGTTTGTAGTCTGCCCGCTGCCCGGTGTCCTC 480
 |||||

RESULT 9
 LOCUS HW21ES27 114 bp mRNA EST 20-SEP-1994
 DEFINITION Homo sapiens expressed sequence tag 21ES0027.
 L25173
 ACCESSION L25173
 NID g540376

Query Match	4.3%	Score 25;	DB 193;	Length 202;
Best Local Similarity	71.9%	Pred.	N.2.10e-07;	
Matches	41;	Conservative	0; Mismatches 16;	Indels 0; Gaps 0;

Db	12	tcttctctctgctccctccgcctcgcgtgatccatccaacagaggatcgccatg	68
Cp	89	TCTTCACCTTCTCCCTCCCTCCACTCTCTTTTCATACAGTCAGTCAAAGCCAIG	33

RESULT	11			EST	19-MAY-1994
LOCUS	T18787	229 bp	mRNA		
DEFINITION	ZET00203-5 Zea mays cDNA clone csuh00203	5'	end.		
FEATURES	T18787				
ACCESSION	G18787				
NID	Q488206				
KEYWORDS	EST.				
SOURCE	maize clone-csuh00203 library=Maize Leaf, Stratagene #937005 strain=B73 vector=Uni-ZAP primer=SK RsiteL-EcoRI Rsite2=XhoI mRNA isolated from illuminated leaves and sheaths of 5 week old plant. cDNA directionally cloned into vector.				

ORGANISM	zma mays
REFERENCE	Eucaryotae; Embryophyta; Magnoliophyta; Liliopsida; Cyperales;
AUTHORS	Poaceae; Zea.
TITLE	1 (bases 1 to 229)
JOURNAL	Baysdorfer,C.
COMMENT	The Maize cDNA Program Unpublished (1993) Contact: Baysdorfer C California State University Dept Biol Sci, California State Univ, Hayward, CA 94542 Tel: 5108813459 Fax: 5107272035 Email: cbaysdor@sl.csu Hayward.edu. Location/Qualifiers 1..229
FEATURES	
source	

/organism="Zea mays" /clone="csuh00203" /strain="B73"										
BASE COUNT		47 a	79 c	52 g	48 t	3 others				
ORIGIN										
Query Match	4.3%	Score 25;	DB 17;	Length 229;						
Best Local Similarity	71.9%;	Pred. No. 2,10e-07;								
Matches	41;	Conservative 0;	Mismatches 16;	Indels 0;	Gaps 0;					
Ddb	19	tattctctctgtctctcgcctcgcctgataccatccagacaggatcccatg	75							
Ccp	89	tcttcaccttcctccctccctccactcctctcttcatacagtcagtaagcccatg	33							
RESULT	12									
LOCUS	T28729	312 bp	mRNA	EST	06-SEP-1995					
DEFINITION	EST53526 Homo sapiens	cDNA 5',	end similar to	erg protein,						
		ets-related (HT11338).								

Euarchyotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Saurpterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 312)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chilu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,J.P.,S., Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaro,S.M., Merrick,J.M., Moreno-Palancues,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.,

REFERENCE
AUTHORS

Saukde,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrile,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji.H., Li.H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence Unpublished (1995)

Contact: Venter, JC

The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423

Email: tdbinfo@tdb.tigr.org

For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfo@tdb.tigr.org).

Location/Qualifiers

1..312

/organism="Homo sapiens"

<1..>312

BASE COUNT 102 a 40 c 99 g 68 t 3 others

ORIGIN

Query Match 4.3%; Score 25; DB 58; Length 312;

Best Local Similarity 83.8%; Pred. No. 2.10e-07;

Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 60 tgaagaaggaggaggaagcagagagaggagagac 96

||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 54 TGAAGAAGGAGGTGGAGGAGGAGGAGGAGGTGAAGAC 90

RESULT 13

LOCUS

DEFINITION Yh75g07.r1 Homo sapiens cDNA clone 135612 5'.

ACCESSION R31397

NID 9787240

KEYWORDS EST.

SOURCE human clone-135612 library-Soares placenta Nb2HP vector-ptT73D

(Pharmacia) with a modified polylinker host-DH10B (ampicillin

resistant) primer-M13RP1 Rsite1-Not I Rsite2-Eco RI Female placenta

obtained at birth (full term). 1st strand cDNA was primed with a

Not I - oligo(dT) primer [5',

ACTGGAAGATTCGGCCGAGGAATTTTTTTTTTTTTTTT 3'], double-stranded

cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the modified pT73

vector. Library went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo.

Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 348)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 259

Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES

source

Location/Qualifiers

1..348

/organism="Homo sapiens"

/clone="135612"

BASE COUNT 118 a 43 c 107 g 79 t 1 others

ORIGIN

Query Match 4.3%; Score 25; DB 23; Length 348;

Best Local Similarity 83.8%; Pred. No. 2.10e-07;

Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 58 tgaagaaggaggaggaagcagagagaggagagac 94

||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 54 TGAAGAAGGAGGTGGAGGAGGAGGAGGAGGTGAAGAC 90

RESULT 14

LOCUS

DEFINITION ye77d06.r1 Homo sapiens cDNA clone 123755 5'.

ACCESSION R01304

NID 9751040

KEYWORDS EST.

SOURCE human clone-123755 library-Soares fetal liver spleen lNPLS

vector-ptT73D (Pharmacia) with a modified polylinker host-DH10B

(ampicillin resistant) primer-M13RP1 Rsite1-Pac I Rsite2-Eco RI

Liver and spleen from a 20 week-post conception male fetus. 1st

strand cDNA was primed with a Pac I - oligo(dT) primer [5',

ACTGGAAGATTAATTAAGACATTTTTTTTTTTTTTTT 3'], double-stranded

cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac

I and cloned into the Pac I and Eco RI sites of the modified pT73

vector. Library went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo.

Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 407)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and

Wilson,R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 264

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Location/Qualifiers

1..407

/organism="Homo sapiens"

/clone="123755"

BASE COUNT 115 a 70 c 117 g 101 t 4 others

ORIGIN

Query Match 4.3%; Score 25; DB 1; Length 407;

Best Local Similarity 83.8%; Pred. No. 2.10e-07;

Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 226 tgaagaaggaggaggaagcagagagaggagagac 262

||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 54 TGAAGAAGGAGGTGGAGGAGGAGGAGGAGGTGAAGAC 90

||||| ||||| ||||| ||||| ||||| ||||| |||||

High quality sequence stops: 259

RESULT 15
 LOCUS W31239 434 bp mRNA EST 20-AUG-1996
 DEFINITION zb45a07.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 306516
 5'
 ACCESSION W31239
 NID g1312231
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 434)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevasakis,E.,
 Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
 WashU-Merck EST Project
 Unpublished (1995)

CONTACT: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 878 Std Error: 0.00
 Seq primer: mob.REGA+ET
 High quality sequence stop: 345.

FEATURES

source
 1..434
 Location/Qualifiers
 /organism="Homo sapiens"
 /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer
 [5'-TGTTCCAACTCTGAAGTGGAGCGCGCAATTTTTTTTTTT-3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldo. This library was constructed
 from the same fetus as the fetal heart library, Soares
 fetal heart NbHL19W."
 /clone="306516"
 /clone_lib="Soares fetal lung NbHL19W"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 <1..>434

BASE COUNT

136 a 68 c 126 g 104 t

Query Match 4.3%; Score 25; DB 128; Length 434;
 Best Local Similarity 83.8%; Pred. NO. 2.10e-07;
 Matches 31; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 179 tgaagaaggaggaggaagagcagaggaaggaggagac 215
 |||||
 QY 54 TGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 90

Search completed on Feb 19 10:11:32 1998
 Job time : 569 secs.

MPSCHPP protein - protein database search, using Smith-Waterman algorithm

(TW)

Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by IntelliGenetics, Inc.
Run on: Thu Feb 19 10:10:06 1998; MasPar time 8.19 Seconds
669.652 Million cell updates/sec
ar output not generated.

Title: >US-08-910-733-13
Description: (1-180) from US08910733.pep
Perfect Score: 1298
Sequence: 1 MALADLYEEGGGGGEGEDN.....LTNPDEGVMVTKFYFQDE 180

Scoring table: PAM 150
Gap 11
Searched: 95051 seqs, 30469580 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: p1r53
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unann11 16:unann12 17:unann13
18:unrev

Statistics: Mean 42.369; Variance 82.094; scale 0.516
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES					Pred. No.	
R	No.	Score	Match	Length	DB ID	Description
1	1298	100.0	180	6	A39386	interleukin-1 recept
2	1140	87.8	177	6	A30368	interleukin-1 recept
3	965	74.3	177	6	A54377	interleukin-1 recept
4	955	73.6	178	6	A44610	interleukin-1 recept
5	905	69.7	178	6	C40956	interleukin-1 recept
6	251	19.3	68	6	B54377	interleukin-1 recept
7	230	17.7	269	2	I53969	interleukin-1 beta p
8	229	17.6	266	2	ICB01B	interleukin-1 beta p
9	228	17.6	266	2	S23010	interleukin-1 beta p
10	214	16.5	267	6	S38373	interleukin-1 beta p
11	205	15.8	267	2	JN0724	interleukin-1 beta p
12	200	15.4	269	2	ICB01B	interleukin-1 beta p
13	195	15.0	268	2	A30584	interleukin-1 beta p
14	96	7.4	370	12	I40358	N-acyl-L-amino acid
15	93	7.2	432	16	A43448	thrombin receptor
16	92	7.1	1024	12	C64208	hypothetical protein
17	91	7.0	490	6	S31450	1-aminocyclopropane
18	89	6.9	219	14	S66947	hypothetical protein
19	89	6.9	396	4	A54536	translation elongati
20	89	6.9	795	8	I50255	108K heat shock prot

21	89	6.9	795	3	HHCH08	heat shock protein 1	2.70e+00
22	88	6.8	157	13	S49793	hypothetical protein	3.61e+00
23	88	6.8	442	1	B4362	protein-tyrosine kin	3.61e+00
24	88	6.8	841	5	S34624	glycogen phosphoryla	3.61e+00
25	88	6.8	842	5	A37335	glycogen phosphoryla	3.61e+00
26	88	6.8	843	1	PHRBG	glycogen phosphoryla	3.61e+00
27	88	6.8	974	5	A49714	protein-tyrosine kin	3.61e+00
28	88	6.8	2317	5	I56752	c-ras-1 tyrosine kin	3.61e+00
29	88	6.8	2338	5	I73957	c-ras-1 tyrosine kin	3.61e+00
30	87	6.7	307	12	G64239	Holliday junction DN	4.81e+00
31	87	6.7	496	6	A47199	1-aminocyclopropane-	4.81e+00
32	87	6.7	496	6	S46189	1-aminocyclopropane-	4.81e+00
33	86	6.6	488	6	JC4549	1-aminocyclopropane-	6.38e+00
34	86	6.6	847	5	A35518	glycogen phosphoryla	6.38e+00
35	84	6.5	244	6	A35227	H+-transporting ATP	1.12e+01
36	84	6.5	362	7	S50993	ribosomal protein L4	1.12e+01
37	84	6.5	362	7	S45887	ribosomal protein L4	1.12e+01
38	85	6.5	387	10	S52274	Nusa protein - Therm	8.46e+00
39	85	6.5	481	12	S69808	lincomycin resistanc	8.46e+00
40	84	6.5	803	8	A35954	endoplasmic precurs	1.12e+01
41	84	6.5	804	8	S51358	protein kinase ppk98	1.12e+01
42	84	6.5	804	8	A53211	glucose-regulated pr	1.12e+01
43	84	6.5	1522	14	S48904	probable purine nucl	1.12e+01
44	83	6.4	336	14	S52691	probable membrane pr	1.47e+01
45	83	6.4	1411	14	S55123	hypothetical protein	1.47e+01

ALIGNMENTS

RESULT 1
ENTRY #type complete
TITLE interleukin-1 receptor antagonist, long intracellular splice
CONTAINS interleukin-1 receptor antagonist, short intracellular splice
ORGANISM #formal_name Homo sapiens #common_name man
DATE 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change
ACCESSIONS I37893; A39386
REFERENCE I37893
#authors Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Mantovani, A.; Colotta, F.
#journal J. Exp. Med. (1995) 182:623-628
#title Cloning and characterization of a new isoform of the interleukin 1 receptor antagonist.
#cross-references MUID:95355865
#accession I37893
#status translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-180 #label RES
#cross-references EMBL:X84348; NID:g1008970; CDS_PID:g1008971
REFERENCE A39386
#authors Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.J.; Hammerberg, C.; Sporn, S.A.; Fong, S.; Arend, W.P.; Ralph, P.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:3681-3685
#title cDNA cloning of an intracellular form of the human interleukin 1 receptor antagonist associated with epithelium.
#cross-references MUID:91219436
#accession A39386
#molecule_type mRNA
#residues 1-3,25-180 #label HAS
#cross-references GB:M55646
GENETICS
#gene GDB:IL1RN
#map_position 2q14.2-2q14.2
CLASSIFICATION #superfamily interleukin-1
KEYWORDS alternative splicing; cytokine receptor
FEATURE
1-180 #product interleukin-1 receptor antagonist, long intracellular splice form #status predicted #label

```

1-3,25-180
SUMMARY
Query Match 100.0%; Score 1298; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.11e-247; Indels 0; Gaps 0;
Matches 180; Conservative 0; Mismatches 0;

Db 1 maladiyeeggggednadsketicrpsgrksskmqafriwdvngktfyrlnnqlva 60
QY 1 MALADLYEEGGGGEGEDNADSKETICRPSGRKSSKMQAFRIWDVNGKTFYRLNNQLVA 60

Db 61 gylgpnvnleekidvvpiephalfihggkmlscvksdetrqlgleavnitdlsenr 120
QY 61 GYLQGPVNVEEKIDVVPIEPHALFLIHGGKMLSCVKSDETRQLGLEAVNITDLSNR 120

Db 121 kqdkrfafirsdsgpttsfesaacpgwflctameadqpsvltmnpdegvmvttkfyfgede 180
QY 121 KQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPSVLTNMPDEGMVMTKIFYQEDE 180

RESULT 2
ENTRY #A30368 #type complete
TITLE interleukin-1 receptor antagonist secreted form precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-May-1997
ACCESSION A40956; I37894; A30368; S08160; S08159; A37822
REFERENCE #authors Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, R.C.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:5232-5236
#title Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family: evolution of a cytokine control mechanism.
#cross-references MUID:91271363
#accession A40956
#molecule_type DNA
#residues 1-177 #label EIS
#cross-references GB:M63099
REFERENCE I37894
#authors Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solar, R.
#journal Cytokine (1992) 4:83-89
#title Cloning and chromosome mapping of the human interleukin-1 receptor antagonist gene.
#cross-references MUID:92338323
#accession I37894
#status translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-177 #label LEN
#cross-references EMBL:X64532; NID:g33798; CDS_PID:g33799
REFERENCE A30368
#authors Carter, D.B.; Deibel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slighcom, J.L.; Berger, A.E.; Bienkowski, M.J.; Sun, F.F.; McEwan, R.N.; Harris, P.K.W.; Yem, A.W.; Waszak, G.A.; Chosay, J.G.; Sieu, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrichson, R.L.; Truesdell, S.E.; Shelly, J.A.; Eessalu, T.E.; Taylor, B.M.; Tracey, D.E.
#journal Nature (1990) 344:633-638
#title Purification, cloning, expression and biological characterization of an interleukin-1 receptor antagonist protein.
#cross-references MUID:90220867
#accession A30368
#molecule_type mRNA
#residues 1-177 #label CAR
#cross-references GB:X53296
#note parts of this sequence, including the amino end of the mature protein, were confirmed by peptide sequencing

```

```

REFERENCE S08160
#authors Eisenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.; Thompson, R.C.
#journal Nature (1990) 343:341-346
#title Primary structure and functional expression from complementary DNA of a human interleukin-1 receptor antagonist.
#cross-references MUID:90136921
#accession S08160
#status not compared with conceptual translation
#molecule_type mRNA
#residues 1-177 #label E12
REFERENCE S08159
#authors Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Dripps, D.J.; Heimdal, P.L.; Armes, L.G.; Sommer, A.; Eisenberg, S.P.; Thompson, R.C.
#journal Nature (1990) 343:336-340
#title Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor.
#cross-references MUID:90136920
#accession S08159
#molecule_type protein
#residues 26-75;97-108;110-116;120-131;163-176 #label HAN
REFERENCE A37822
#authors Bienkowski, M.J.; Eessalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde, A.L.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrichson, R.L.; Chosay, J.G.; Tracey, D.E.
#journal J. Biol. Chem. (1990) 265:14505-14511
#title Purification and characterization of interleukin 1 receptor level antagonist proteins from THP-1 cells.
#cross-references MUID:90354444
#accession A37822
#molecule_type protein
#residues 26-52;70-77;122-127;170-175 #label BIE
#experimental_source culture medium, PMA-stimulated THP-1 cells
GENETICS
#gene GDB:IL1RN
#cross-references GDB:125897
#map_position 2q14.2-2q14.2
#introns 39/2; 69/1; 106/3
CLASSIFICATION #superfamily interleukin-1
KEYWORDS alternative splicing; cytokine receptor; extracellular protein; glycoprotein
FEATURE
1-25 #domain signal sequence #status experimental #label SIG
26-177 #product interleukin-1 receptor antagonist #status experimental #label MAT
109 #binding_site carbohydrate (Asn) (covalent) #status experimental
SUMMARY #length 177 #molecular-weight 20055 #checksum 193
Query Match 87.8%; Score 1140; DB 6; Length 177;
Best Local Similarity 100.0%; Pred. No. 5.41e-213; Indels 0; Gaps 0;
Matches 156; Conservative 0; Mismatches 0;
Db 22 eticrpsgrksskmqafriwdvngktfyrlnnqlvavgpvnleekidvvpiephal 81
QY 25 ETICRPSGRKSSKMQAFRIWDVNGKTFYRLNNQLVAGLPVNVLEEKIDVVPIEPHAL 84
Db 82 flghggkmlscvksdetrqlgleavnitdlsenrkqdkrfafirsdsgpttsfesaac 141
QY 85 FLGHGGKMLSCVKSDETRQLGLEAVNITDLSNRKQDKRFAFIRSDSGPTTSFESAAC 144
Db 142 pgwflctameadqpsvltmnpdegvmvttkfyfgede 177
QY 145 PGWFLCTAMEADQPSVLTNMPDEGMVMTKIFYQEDE 180
RESULT 3
ENTRY #A54377 #type complete
TITLE interleukin-1 receptor antagonist secreted form precursor - rabbit
ORGANISM #formal_name Oryctolagus cuniculus #common_name domestic

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```

rabbit
06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
23-May-1997
A54377; I46729
REFERENCE
#authors
Cominelli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.;
Ferretti, M.; Brewer, M.T.; Eisenberg, S.P.; Ng, R.K.
#journal
J. Biol. Chem. (1994) 269:6962-6971
#title
Rabbit interleukin-1 receptor antagonist. Cloning,
expression, functional characterization, and regulation
during intestinal inflammation.
#cross-references MUID:94165101
#accession A54377
#molecule_type mRNA
#residues 1-177 #label COM
#cross-references NCBI:144168; NCBI:144169
#experimental_source colon tissue
#note
I46729 sequence extracted from NCBI backbone
REFERENCE
#authors
Goto, F.; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.;
Mori, S.; Furukawa, S.; Maeda, T.; Iwanaga, S.; Shimonishi,
Y.; Yoshinaga, M.
Immunology (1992) 77:235-244
Interleukin-1 receptor antagonist in inflammatory exudate
cells of rabbits. Production, purification and
determination of primary structure.
#cross-references MUID:93052512
#accession I46729
#status translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-177 #label GOT
#cross-references GB:D1832; NID:g425787; CDS_PID:g452205
CLASSIFICATION
#superfamily interleukin-1
KEYWORDS
cytokine receptor; extracellular protein; glycoprotein
FEATURE
1-25
109
#domain signal sequence #status predicted #label SIG\
#binding_site carbohydrate (Asn) (covalent) #status
predicted
SUMMARY
#length 177 #molecular-weight 20214 #checksum 847
Query Match 74.3%; Score 965; DB 6; Length 177;
Best Local Similarity 78.2%; Pred. No. 2.82e-175;
Matches 122; Conservative 24; Mismatches 10; Indels 0; Gaps 0;
Db 22 etacpgrkprcmqafriwvqkfylnqvlvqyqgpnakleeridvvpqll 81
QY 25 ETICRPSGRKSKMqAFRIWDVYVQKTFYLRNQLVAGYVQGNVLEKIDVVPIDPHAL 84
Db 82 flglgrklclscvsgdkmklhlaevntldlgkneqdkfrfirsngpttffesasc 141
QY 85 FLGIHGRKMLCVKSGDTRQLQLEAVNTDLSENKQDKRFAFIRSDSGPTTSFESAC 144
Db 142 pwfictaleadqpsltnpddsiwvtfkyfqedq 177
QY 145 PGWFLCTAMEADQPSVLTNMPDEGVMTREYFQEDE 180

RESULT 4
ENTRY
TITLE interleukin-1 receptor antagonist precursor - mouse
ALTERNATE_NAMES IL-1Ra
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change
23-May-1997
A44610; B40956; A49031; I56106; I52970
REFERENCE
A44610
#authors
Matsushima, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.;
Sherr, C.J.
#journal
Blood (1991) 78:616-623
#title
Cloning and expression of murine interleukin-1 receptor
antagonist in macrophages stimulated by colony-stimulating
factor 1.
#accession A44610

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#molecule_type mRNA
#residues 1-178 #label MAT
#cross-references GB:M64404
REFERENCE
A40956
#authors
Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.;
Brandhuber, B.J.; Thompson, R.C.
#journal
Proc. Natl. Acad. Sci. U.S.A. (1991) 88:5232-5236
#title
Interleukin 1 receptor antagonist is a member of the
interleukin 1 gene family: evolution of a cytokine control
mechanism.
#cross-references MUID:91271363
#accession B40956
#molecule_type DNA
#residues 7-178 #label EIS
#cross-references GB:M63100
REFERENCE
A49031
#authors
Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.
#journal
Eur. J. Immunol. (1991) 21:2775-2780
#title
Cloning, heterologous expression and characterization of
murine interleukin 1 receptor antagonist protein.
#cross-references MUID:92037824
#accession A49031
#molecule_type mRNA
#residues 23-178 #label SHU
#cross-references NCBI:64082; NCBI:64085
#experimental_source peritoneal macrophages, ICR strain
#note
sequence extracted from NCBI backbone
REFERENCE
I56106
#authors
Zahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.;
Whitehead, A.S.
#journal
J. Immunol. (1991) 146:4228-4233
#title
Mouse IL-1 receptor antagonist protein: Molecular
characterization, gene mapping, and expression of mRNA in
vitro and in vivo.
#cross-references MUID:91250712
#accession I56106
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-178 #label RES
#cross-references GB:M74294; NID:g198387; CDS_PID:g198388
REFERENCE
I52970
#authors
Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead,
A.S.
#journal
Cytokine (1994) 6:1-9
#title
The mouse interleukin 1 receptor antagonist protein: gene
structure and regulation in vitro.
#cross-references MUID:94271931
#accession I52970
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-178 #label RE2
#cross-references GB:L32838; NID:g487864; CDS_PID:g528978
GENETICS
#gene IL-1rn
#introns 40/2; 70/1; 107/3
CLASSIFICATION
#superfamily interleukin-1
KEYWORDS
cytokine receptor
FEATURE
1-26
27-178
#domain signal sequence #status predicted #label SIG\
#product interleukin-1 receptor antagonist #status
predicted #label MA2
SUMMARY
#length 178 #molecular-weight 20274 #checksum 8941
Query Match 73.6%; Score 955; DB 6; Length 178;
Best Local Similarity 76.3%; Pred. No. 3.96e-173;
Matches 119; Conservative 25; Mismatches 12; Indels 0; Gaps 0;
Db 23 eaacpgrkprcmqafriwvqkfylnqvlvqyqgpnakleeridvvpqllhsv 82
QY 25 ETICRPSGRKSKMqAFRIWDVYVQKTFYLRNQLVAGYVQGNVLEKIDVVPIDPHAL 84
Db 83 flglhgrklclscvsgdkmklhlaevntldlgkneqdkfrfirsngpttffesaac 142

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KEYWORDS      cytokine receptor
SUMMARY       #length 68 #checksum 2056

Query Match   19.3%; Score 251; DB 6; Length 68;
Best Local Similarity 79.5%; Pred. No. 2,20e-27;
Matches 31; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Ddb          30 asetacrpqkpcrmqafriwdvngktfyrlnnqlvag 68
              : || |||||::: ||||||||| ||||||||| |||||
QY           23 SKETICRPSGRKSKMQAFRIWDVNGKTFLYRNQLVAG 61

RESULT 7
ENTRY    IL5969          #type complete
TITLE    Interleukin-1 beta precursor - mouse
ALTERNATE_NAMES hematoipoietin-1; IL-1 beta
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE     26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change
         16-Feb-1997
ACCESSIONS I5969; A24719; S13029
REFERENCE   I5969
AUTHORS    Gray, P.W.; Glaister, D.; Chen, E.; Goeddel, D.V.; Pennica,
            D.
#journal   J. Immunol. (1986) 137:3644-3648
#title     Two interleukin 1 genes in the mouse: Cloning and expression
            of the cDNA for murine interleukin 1-beta.
#crosso-references MUID:87058957
#accession  I5969
##status    preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues  1-269 ##label RES
##crosso-references GB:M15131; NID:g198293; CDS_PID:g309398
REFERENCE   A24719
AUTHORS    Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla,
            E.; Melli, M.
#journal   Nucleic Acids Res. (1986) 14:9955-9963
#title     The murine interleukin 1-beta gene: structure and evolution.
#crosso-references MUID:87117546
#accession  A24719
##molecule_type mRNA
##residues  1-269 ##label TEL
REFERENCE   S13029
AUTHORS    Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColl, A.S.;
            Geoghegan, K.F.; Otterness, I.G.
#journal   FBS Lett. (1991) 278:98-102
#title     Reduction of biological activity of murine recombinant
            interleukin-1beta by selective deamidation at
            asparagine-149.
#crosso-references MUID:91130610
#accession  S13029
##status    preliminary
##molecule_type protein
##residues  118-269 #label DAU
COMMENT     This protein lacks a conventional signal sequence for protein
            export. Cleavage of a long N-terminal propeptide occurs with
            secretion, although uncleaved forms are also released. The
            uncleaved form of interleukin-beta, unlike interleukin 1-alpha,
            is inactive.
COMMENTS    Interleukin-beta precursor is less heavily myristoylated than
            interleukin-1alpha precursor.

GENETICS
#gene      IL-1-beta
CLASSIFICATION #superfamily interleukin-1
KEYWORDS     cytokine; immunoregulation; inflammation; lymphokine;
            macrophage; mitogen
FEATURE
#feature    #product interleukin-1 beta #status experimental #label
            111
SUMMARY     #length 269 #molecular-weight 30931 #checksum 8753

Query Match   17.7%; Score 230; DB 2; Length 269;
Best Local Similarity 30.7%; Pred. No. 1.84e-23;
Matches 42; Conservative 34; Mismatches 53; Indels 8; Gaps 7;

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Query Match	17.6%;	Score	229;	DB	2;	Length	265;
Best Local Similarity	37.1%;	Pred. No.	2,82e-23;				
Matches	33;	Conservative	17;	Mismatches	37;	Indels	2;
Gaps	2;						
173	lqikdnlylscvckgddptlqleavd-pkvyppkrmekrfvfykteiknkvfesvlyp	231		:::		:::	
86	LGIHGGKCLSCVKSGETRLQLEAVNTDLSENRKRQKRFARIRSDSGPTTFESAACP	145		:::		:::	
232	nwyistsgleerpfvflghfrg-ggditdf	259		:::		:::	
146	GWFLCTAMEADQPVSLTNNPDEGVAVTKF	174		:::		:::	
RESULT	9	S23010	#type	complete			
ENTRY							

RESULT	9	
ENTRY	S23010	#type complete

```

RESULT 10
ENTRY
TITLE Interleukin-1 beta precursor - pig
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE 20-May-1994 #sequence_revision 01-Dec-1995 #text_change
03-May-1996

ACCESSIONS S38373
REFERENCE S38373
#authors Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.;
Janssen, A.; van Damme, J.; Opdenakker, G.; Billiau, A.
#journal Eur. J. Biochem. (1993) 217:45-52
#title Gene sequence, cDNA construction, expression in Escherichia
coli and genetically approached purification of porcine
interleukin-1-beta.
#accession S38373
##status preliminary
##molecule_type DNA
##residues 1-267 ##label VAN
##cross-references EMBL:X74568
CLASSIFICATION
INTRONS 16/2; 33/3; 99/1; 154/1; 197/3
#superfamily interleukin-1
SUMMARY #length 267 #molecular-weight 29893 #checksum 8512

Query Match 16.5%; Score 214; DB 6; Length 267;
Best Local Similarity 38.5%; Pred. No. 1.60e-20;
Matches 30; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

Db 174 lgikgnlyscvmdktdptlqlkdvpkyp-krdmekrfvfykteknrvfesalyp 232
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
86 LGIHGKMLCVKSGDTRQLQLEAVNITDLSNRKQKRFATKSDGPTTSFESAACP 145
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 233 nwyistsaqekpvlfn 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 146 GWFLCTAMEADQPVSILN 163
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
ENTRY
TITLE Interleukin-1 beta precursor - pig
ALTERNATE_NAMES hematopoietin-1; IL-1 beta
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change
16-Feb-1997

ACCESSIONS JN0724
REFERENCE JN0724
#authors Huether, M.J.; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor,
T.W.
#journal Gene (1993) 129:285-289
#title Cloning, sequencing and regulation of an mRNA encoding
porcine interleukin-1 beta.
#accession JN0724
##molecule_type mRNA
##residues 1-267 ##label HUE
##cross-references GB:M86725
##experimental_source alveolar macrophage
COMMENT This protein is a pleiotropic cytokine that mediates a variety of
processes in host defense, inflammation, and response to injury.
This protein lacks a conventional signal sequence for protein
export. Cleavage of a long N-terminal propeptide occurs with
secretion, although uncleaved forms are also released. The
uncleaved form of interleukin-1beta, unlike interleukin 1-alpha,
is inactive.
COMMENT Interleukin-1beta precursor is less heavily myristoylated than
interleukin-1alpha precursor.
CLASSIFICATION #superfamily interleukin-1
KEYWORDS cytokine; immunoregulation; inflammation; lymphokine;
macrophage; mitogen
FEATURE
115-267 #product interleukin-1 beta #status predicted #label
IL1
77 #binding_site myristate (1ys) (covalent) #status
predicted

```

```

SUMMARY #length 267 #molecular-weight 30404 #checksum 9362

Query Match 15.8%; Score 205; DB 2; Length 267;
Best Local Similarity 35.9%; Pred. No. 6.87e-19;
Matches 28; Conservative 16; Mismatches 33; Indels 1; Gaps 1;

Db 174 lgikgnlyscvmdktdptlqlkdvpkyp-krdmekrfvfykteknrvfesalyp 232
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
86 LGIHGKMLCVKSGDTRQLQLEAVNITDLSNRKQKRFATKSDGPTTSFESAACP 145
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 233 nwyistsaqekpvlfn 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 146 GWFLCTAMEADQPVSILN 163
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
ENTRY
TITLE Interleukin-1 beta precursor - human
ALTERNATE_NAMES hematopoietin-1; IL-1 beta
ORGANISM #formal_name Homo sapiens #common_name man
DATE 28-Feb-1986 #sequence_revision 28-May-1986 #text_change
16-Feb-1997
ACCESSIONS A25542; A29019; A94023; A93361; B27616; I51852; I65200;
I38132; A01848; S19626
REFERENCE A25542
#authors Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron,
P.E.
#journal Nucleic Acids Res. (1986) 14:7897-7914
#title Genomic sequence for human prointerleukin 1 beta: possible
evolution from a reverse transcribed prointerleukin 1 alpha
gene.
#cross-references MUID:87040762
#accession A25542
##molecule_type DNA
##residues 1-269 ##label CLA
##cross-references GB:X04500
REFERENCE A29019
#authors Bensi, G.; Raugi, G.; Palla, E.; Carinci, V.; Buonamassa,
D.T.; Melli, M.
#journal Gene (1987) 52:95-101
#title Human interleukin-1 beta gene.
#cross-references MUID:87248099
#accession A29019
##molecule_type DNA
##residues 1-5, 'E', 7-269 ##label BEN
##cross-references GB:M15840
REFERENCE A94023
#authors Auron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.;
Rich, A.; Wolff, S.M.; Dinarello, C.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:7907-7911
#title Nucleotide sequence of human monocyte interleukin 1 precursor
cDNA.
#cross-references MUID:85088517
#accession A94023
##molecule_type mRNA
##residues 1-269 ##label AUR
##cross-references GB:X02770
REFERENCE A93361
#authors March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt,
G.; Price, V.; Gillis, S.; Henney, C.S.; Kronheim, S.R.;
Grabstein, K.; Conlon, P.J.; Hopp, T.P.; Cosman, D.
#journal Nature (1985) 315:641-647
#title Cloning, sequence and expression of two distinct human
interleukin-1 complementary DNAs.
#cross-references MUID:85240547
#accession A93361
##molecule_type mRNA
##residues 1-5, 'E', 7-269 ##label MAR
##cross-references GB:X02532
##note parts of this sequence, including the amino end of the
mature form, were confirmed by peptide sequencing;
confirmed absence of glycosylation at 123-Asn
REFERENCE A90732

```

#authors Zsebo, K.M.; Wypych, J.; Yushchenko, V.N.; Lu, H.; Hunt, P.;
 #journal Dukes, P.P.; Langley, K.E.
 #title Blood (1988) 71:962-968
 #cross-references MUID:88184226
 #accession B27616
 #molecule_type protein
 #residues 117-123, 'X', 125-126, 'X', 128 #label ZSE
 REFERENCE S19608
 #authors Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Kilian, P.L.;
 Stern, A.S.
 #journal Biochim. Biophys. Acta (1991) 1118:25-35
 #title The role of arginine residues in interleukin 1 receptor binding.
 #cross-references MUID:92110334
 #contents annotation; type 1 IL-1 receptor interaction site
 #note modification of Arg-120 by phenylglyoxal blocks receptor binding
 REFERENCE A44666
 #authors Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.;
 Watenpaugh, K.D.; Einspahr, H.M.
 #journal J. Mol. Biol. (1989) 209:779-791
 #title Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom resolution.
 #contents annotation; X-ray crystallography, 2.0 angstroms
 #authors A44675
 #journal Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.
 #title Biochemistry (1991) 30:2315-2323
 #cross-references MUID:92110334
 #contents annotation; type 1 IL-1 receptor interaction site
 #note modification of Arg-120 by phenylglyoxal blocks receptor binding
 REFERENCE A44675
 #authors Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.;
 Rich, A.C.; Wolff, S.M.; Auer, P.E.
 #journal Adv. Gene Technol. (1985) 22:339-340
 #title Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
 #accession I51852
 #status translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269
 #cross-references GB:M54933; NID:g186287; CDS_PID:g186288
 REFERENCE I52217
 #authors Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.;
 Masui, Y.; Nakai, S.; Hirai, Y.
 #journal Biochem. Biophys. Res. Commun. (1987) 143:345-352
 #title cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
 #cross-references MUID:87156769
 #accession I65200
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-5, 'E', 7-269 #label RE2
 #cross-references GB:M15330; NID:g186283; CDS_PID:g307045
 REFERENCE I38131
 #authors Kotenko, S.V.; Buleikov, M.T.; Veiko, V.P.; Epishin, S.M.;
 Lomakin, I.B.; Emel'yanov, A.V.; Kozlov, A.P.; Konusova, V.G.; Kotov, A.Y.; Kurbatova, T.V.; Reshetnikov, V.L.;
 Simbirtsev, A.S.; Ketlinskii, S.A.; Vinetskii, Y.P.
 #journal Dokl. Akad. Nauk SSSR (1989) 309:1005-1008
 #title [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin-1 beta].
 #cross-references MUID:90249285
 #accession I38132
 #status translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-5, 'E', 7-269 #label RE3
 #cross-references EMBL:X56087; NID:g35662; CDS_PID:g35663
 REFERENCE A48293
 #authors Stevenson, F.T.; Burston, S.L.; Fanton, C.; Locksley, R.M.;

Lovett, D.H.
 Proc. Natl. Acad. Sci. U.S.A. (1993) 90:7245-7249
 #journal The 31-kDa precursor of interleukin 1alpha is myristoylated
 #title on specific lysines within the 16-kDa N-terminal propeptide.
 #cross-references MUID:88184226
 #accession A39774
 #molecule_type protein
 #residues 117-269
 #status translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269
 #cross-references GB:M54933; NID:g186287; CDS_PID:g186288
 REFERENCE I52217
 #authors Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.;
 Masui, Y.; Nakai, S.; Hirai, Y.
 #journal Biochem. Biophys. Res. Commun. (1987) 143:345-352
 #title cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
 #cross-references MUID:87156769
 #accession I65200
 #status preliminary; translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-5, 'E', 7-269 #label RE2
 #cross-references GB:M15330; NID:g186283; CDS_PID:g307045
 REFERENCE I38131
 #authors Kotenko, S.V.; Buleikov, M.T.; Veiko, V.P.; Epishin, S.M.;
 Lomakin, I.B.; Emel'yanov, A.V.; Kozlov, A.P.; Konusova, V.G.; Kotov, A.Y.; Kurbatova, T.V.; Reshetnikov, V.L.;
 Simbirtsev, A.S.; Ketlinskii, S.A.; Vinetskii, Y.P.
 #journal Dokl. Akad. Nauk SSSR (1989) 309:1005-1008
 #title [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin-1 beta].
 #cross-references MUID:90249285
 #accession I38132
 #status translated from GB/EMBL/DBJ
 #molecule_type mRNA
 #residues 1-5, 'E', 7-269 #label RE3
 #cross-references EMBL:X56087; NID:g35662; CDS_PID:g35663
 REFERENCE A48293
 #authors Stevenson, F.T.; Burston, S.L.; Fanton, C.; Locksley, R.M.;


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#authors      Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schweissner, U.;
#journal      J. Immunol. (1989) 142:2299-2306
#title       Rabbit IL-1. Cloning, expression, biologic properties, and
#             transcription during endotoxemia.
#cross-references MUID:89176242
#accession     A30584
##molecule_type mRNA
##residues     1-268 ##label CAN
REFERENCE      A94230
#authors      Young, P.R.; Sylvester, D.
#journal      Protein Eng. (1989) 2:545-551
#title       Cloning of rabbit interleukin-1 beta: differential evolution
#             of IL-1 alpha and IL-1 beta proteins.
#cross-references MUID:89315718
#accession     JU0082
##molecule_type mRNA
##residues     1-268 ##label YOU
COMMENT       This protein lacks a conventional signal sequence for protein
              export. Cleavage of a long N-terminal propeptide occurs with
              secretion, although uncleaved forms are also released. The
              uncleaved form of interleukin-1beta, unlike interleukin 1-alpha,
              is inactive.
COMMENT       Interleukin-1beta precursor is less heavily myristoylated than
              interleukin-1alpha precursor.
CLASSIFICATION superfamily interleukin-1
KEYWORDS       cytokine; immunoregulation; inflammation; lymphokine;
              macrophage; mitogen
FEATURE
117-268       #product interleukin-1 beta #status predicted #label ILB
SUMMARY       #length 268 #molecular-weight 30665 #checksum 3461

Query Match      15.0%; Score 195; DB 2; Length 268;
Best Local Similarity 37.2%; Pred. No. 4.27e-17;
Matches 29; Conservative 16; Mismatches 32; Indels 1; Gaps 1;

Db 175 lgirgklyiscvnmkdkptqlqlesvd-pnryppkkmekrfvfkielekdklefesagfp 233
QY 86 LGIHGGRKCLSCVKSGDETRQLQLEAVNITLSENKQDKRFARISDSGPTTSFESAACP 145
Db 234 nwyistsqtymypvflgn 251
QY 146 GWFLCTAEADQPVSLTN 163

RESULT 14
ENTRY   I40358 #type complete
#authors      Sakanyan, V.; Desmarez, L.; Legrain, C.; Charlier, D.; Mett,
              T.; Kochikyan, A.; Savchenko, A.; Boyen, A.; Falmagne, P.;
              Pirard, A.; Glansdorff, N.
#journal      Appl. Environ. Microbiol. (1993) 59:3878-3888
#title       Gene cloning, sequence analysis, purification, and
              characterization of a thermostable aminoacylase from
              Bacillus stearothermophilus.
#cross-references MUID:94113715
#accession     I40358
##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues     1-370 #label RES
##cross-references EMBL:X74289; NID:g436795; CDS_PID:g436797
GENETICS
#gene         ama
SUMMARY       #length 370 #molecular-weight 41676 #checksum 5132

Query Match      7.4%; Score 96; DB 12; Length 370;
Best Local Similarity 25.3%; Pred. No. 3.36e-01;

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Matches 20; Conservative 23; Mismatches 30; Indels 6; Gaps 6;

Db 64 rli-gqgprvairadmdalpiqentfefasknpgvm-hacghdghtaml-lgtakif 120
QY 57 QLVAGVLPQPNVNLKIDVPI-EPHAL-FLGIHGKMKCLSCVKSGDETRQLQLEAVNI- 113
Db 121 sqldrdirgeirflfqhae 139
QY 114 TDLSENKQDKRFARISD 132

RESULT 15
ENTRY   A43448 #type complete
#authors      thrombin receptor - rat
#journal      #formal_name Rattus norvegicus #common_name Norway rat
#title       04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
              16-Feb-1997
ACCESSIONS    A43448
REFERENCE      A43448
#authors      Zhong, C.; Hayzer, D.J.; Corson, M.A.; Runge, M.S.
#journal      J. Biol. Chem. (1992) 267:16975-16979
#title       Molecular cloning of the rat vascular smooth muscle thrombin
              receptor. Evidence for in vitro regulation by basic
              fibroblast growth factor.
#cross-references MUID:92381002
#accession     A43448
##status      preliminary
##molecule_type mRNA
##residues     1-432 ##label ZHO
##cross-references NCBI:111973; NCBI:111974
##experimental_source RASM aortic smooth muscle cells
##note         sequence extracted from NCBI backbone
KEYWORDS       G protein-coupled receptor; transmembrane protein
SUMMARY       #length 432 #molecular-weight 48280 #checksum 6313

Query Match      7.2%; Score 93; DB 16; Length 432;
Best Local Similarity 35.0%; Pred. No. 8.33e-01;
Matches 14; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

Db 43 nprsfllrnp-edtfefpigdeeknesiplegayvl 81
QY 47 NQRTFLRNQLVAGYLOGPNVNLEEKIDVVPTEPHALFL 86

Search completed: Thu Feb 19 10:10:36 1998
Job time : 30 secs.

```

M P S R C H
***** (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Feb 19 10:10:54 1998; MasPar time 5.54 Seconds
689.392 Million cell updates/sec
No output not generated.

Title: >US-08-910-733-13
Description: (1-180) from US08910733.pap
Perfect Score: 1298
Sequence: 1 MALADLYEKGGGGGEGEDN.....LTNMPDEGVMVTKFYQDE 180

Scoring table: PAM 150
Gap 11

Searched: 59021_seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 43.764; Variance 70.225; scale 0.623

Pred..No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description	Pred. No.
1	1140	87.8	177	5	IL1X_HUMAN INTERLEUKIN-1 RECEPTO	1.48e-256
2	965	74.3	177	5	IL1X_RABIT INTERLEUKIN-1 RECEPTO	4.31e-211
3	955	73.6	178	5	IL1X_MOUSE INTERLEUKIN-1 RECEPTO	1.67e-208
4	905	69.7	178	5	IL1X_RAT INTERLEUKIN-1 RECEPTO	1.39e-195
5	230	17.7	269	5	IL1B_MOUSE INTERLEUKIN-1 BETA PR	1.85e-28
6	229	17.6	266	5	IL1B_BOVIN INTERLEUKIN-1 BETA PR	3.09e-28
7	228	17.6	266	5	IL1B_SHEEP INTERLEUKIN-1 BETA PR	5.13e-28
8	223	17.2	266	5	IL1B_CEREL INTERLEUKIN-1 BETA PR	6.50e-27
9	205	15.8	267	5	IL1B_PIG INTERLEUKIN-1 BETA PR	5.41e-23
10	202	15.6	269	5	IL1B_MACMU INTERLEUKIN-1 BETA PR	2.39e-22
11	202	15.6	269	5	IL1B_MACNE INTERLEUKIN-1 BETA PR	2.39e-22
12	200	15.4	269	5	IL1B_HUMAN INTERLEUKIN-1 BETA PR	6.42e-22
13	198	15.3	267	5	IL1B_FELCA INTERLEUKIN-1 BETA PR	1.72e-21
14	195	15.0	268	5	IL1B_RABIT INTERLEUKIN-1 BETA PR	7.49e-21
15	184	14.2	269	5	IL1B_CERTO INTERLEUKIN-1 BETA PR	1.57e-18
16	96	7.4	370	1	AMA_BACST N-ACYL-L-AMINO ACID A	5.25e-02
17	93	7.2	432	9	THRR_RAT THROMBIN RECEPTOR PRE	1.51e-01
18	92	7.1	1024	10	Y075_MYGE HYPOTHETICAL PROTEIN	2.14e-01
19	89	6.9	320	9	SOX2_SHEEP SOX-2 PROTEIN	5.97e-01
20	89	6.9	396	3	EFTU_FLESI ELONGATION FACTOR TU	5.97e-01
21	89	6.9	795	3	ENPL_CHICK ENDOPLASMIN PRECURSOR	5.97e-01
22	88	6.8	157	11	YII7_YEAST HYPOTHETICAL 16.9 KD	8.35e-01

RESULT	ID	IL1X_HUMAN	STANDARD;	PRT;	177 AA.
AC	PI8510;				
DT	01-NOV-1990	(REL. 16, CREATED)			
DT	01-NOV-1990	(REL. 16, LAST SEQUENCE UPDATE)			
DT	01-FEB-1996	(REL. 33, LAST ANNOTATION UPDATE)			
DE	INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL-1RA) (IRAP).				
GN	IL1RN OR IL1RA.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 90220867.				
RA	CARTER D.B., DEIBEL M.R. JR., DUNN C.J., TOMICH C.S.C., LABORDE A.L., SLIGHTOM J.L., BERGER A.E., BIENKOWSKI M.J., SUN F.F., MCEWAN R.N., HARRIS P.K.W., YEM A.W., WASZAK G.A., CHOSAY J.G., SIEU L.C., HARDEE M.M., ZURCHER-NEELY H.A., REARDON I.M., HEINRIKSON R.L., TRUESDELL S.E., SHELLY J.A., EESSALU T.E., TAYLOR B.M., TRACEY D.E.;				
RL	NATURE 344:633-638(1990).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 90136921.				
RA	EISENBERG S.P., EVANS R.J., AREND W.P., VERDERBER E., BREWER M.T., HANNUM C.H., THOMPSON R.C.;				
RL	NATURE 343:341-346(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 91271363.				
RA	EISENBERG S.P., BREWER M.T., VERDERBER E., HEIMDAL P., BRANDHUBER B.J., THOMPSON R.C.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 88:5232-5236(1991).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 92338323.				
RA	LENNARD A., GORMAN P., CARRIER M., GRIFFITHS S., SCOTNEY H., SHEER D., SOLARI R.;				
RL	CYTOKINE 4:83-89(1992).				
RN	[5]				
RP	SEQUENCE OF 26-45.				
RX	MEDLINE; 90136920.				
RA	HANNUM C.H., WILCOX C.J., AREND W.P., JOSLIN F.G., DRIPPS D.J., HEIMDAL P.L., ARMES L.G., SOMMER A., EISENBERG S.P., THOMPSON R.C.;				
RL	NATURE 343:336-340(1990).				
RN	[6]				

ALIGNMENTS

[illegible]

[illegible]

RL J. IMMUNOL. 140:3838-3843(1988).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE:82222282
 RA VAN OOSTRUM J., PRIESTLE J.P., GRUTTER M.G., SCHMITZ A.;
 RL J. STRUCT. BIOL. 107:189-195(1991).
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -!- SUBUNIT: MONOMER.
 CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 DR EMBL; M15131; G309398; -.
 DR EMBL; X04964; G52667; -.
 DR PIR; A24719; A24719.
 DR PIR; S13029; S13029.
 DR PDB; 811B; 15-OCT-94.
 DR PDB; 2M1B; 31-JAN-94.
 DR PROSITE; PS00253; INTERLEUKIN_1.
 KW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN;
 KW 3D-STRUCTURE.
 FT PROPEP 1 117
 FT CHAIN 118 269 INTERLEUKIN-1 BETA.
 FT CARBOHYD 57 57
 FT CARBOHYD 253 253 POTENTIAL.
 FT STRAND 123 129
 FT TURN 130 131
 FT STRAND 134 137
 FT TURN 140 141
 FT STRAND 143 146
 FT TURN 150 154
 FT STRAND 159 163
 FT TURN 170 171
 FT STRAND 173 179
 FT TURN 180 181
 FT STRAND 184 191
 FT TURN 192 193
 FT STRAND 194 201
 FT TURN 204 206
 FT HELIX 214 216
 FT STRAND 217 222
 FT STRAND 227 231
 FT TURN 235 236
 FT STRAND 238 242
 FT STRAND 247 248
 FT STRAND 250 252
 FT STRAND 258 259
 FT STRAND 262 266
 SQ SEQUENCE 269 AA; 30931 MW; B72ACA9F CRC32;
 Query Match 17.7%; Score 230; DB 5; Length 269;
 Best Local Similarity 30.7%; Pred. No. 1.85e-28;
 Matches 42; Conservative 34; Mismatches 53; Indels 8; Gaps 7;
 Db 125 ylrdeqkslvsdpyelkallhngqinqvifmsfvqgpepsndkipvalgikgnl 184
 QY 41 FRWDVYQKTFYLRNN-QLVAGYLGQPNVLEEKIDV--VPIEP-HA-L-F-LGIHGGKM 93
 Db 185 ylsclvndgtptlqlesvdpkqyp-kkkmekrfvfknievskvfesaeafnpwistsq 243
 QY 94 CLSCVKSGDETRQLQEAVNITDLSNKRQDKRFARFIRSDSGPTTSFESAACPGWFLCTAM 153
 Db 244 aektpvflgnssqddii 260
 QY 154 EADQPVSLTNMPDEGVM 170

RESULT 6
 ID IL1B_BOVIN STANDARD; PRT; 266 AA.
 AC P09438;
 DT 01-MAR-1989 (REL. 10, CREATED)
 DT 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
 GN IL1B.
 OS BOS TAURUS (BOVINE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; ARTIODACTYLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89016591.
 RA LEONG S.R., FLAGGS G.M., LAWMAN M., GRAY P.W.;
 RL NUCLEIC ACIDS RES. 16:9054-9054(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88318652.
 RA MALISZEWSKI C.R., BAKER P.E., SCHOENBORN M.A., DAVIS B.S., COSMAN D.,
 RA GILLIS S., CERRETTI D.P.;
 RL MOL. IMMUNOL. 25:429-437(1988).
 CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -!- SUBUNIT: MONOMER.
 CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 DR EMBL; M35589; G163203; -.
 DR EMBL; X12498; G449; -.
 DR EMBL; M37211; G163201; -.
 DR PIR; JL0010; ICBO1B.
 DR PIR; S01380; S01380.
 DR HSP; P01584; I1H1B.
 DR PROSITE; PS00253; INTERLEUKIN_1.
 KW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.
 FT PROPEP 1 113
 FT CHAIN 114 266 INTERLEUKIN-1 BETA.
 FT CARBOHYD 58 58 POTENTIAL.
 FT CONFLICT 252 252 A -> G (IN REF. 2).
 SQ SEQUENCE 266 AA; 30774 MW; 1DF2785C CRC32;
 Query Match 17.6%; Score 229; DB 5; Length 266;
 Best Local Similarity 37.1%; Pred. No. 3.09e-28;
 Matches 33; Conservative 17; Mismatches 37; Indels 2; Gaps 2;
 Db 173 lgikdknlylscvkkgtptlqleevd-pkvyprkrmekrfvfyktaikntvefsvlyp 231
 QY 86 LGIHGGKMCLSCVKSGDETRQLQEAVNITDLSNKRQDKRFARFIRSDSGPTTSFESAACP 145
 Db 232 nwyistsqleerpyflghfra-gqdltdf 259
 QY 146 GWFLCTAMEADQPVSLTNMPDEGVMVTKF 174
 RESULT 7
 ID IL1B_SHEEP STANDARD; PRT; 266 AA.
 AC P21621;
 DT 01-MAY-1991 (REL. 18, CREATED)
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
 GN IL1B.

CC	THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC	MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC	IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC	IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE
CC	THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC	-!- SUBUNIT: MONOMER.
CC	-!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO
CC	ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC	-!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
CC	SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS
CC	SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC	SECRETORY PROTEINS.
CC	-!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC	EMBL: U20500; G665946; -.
KW	CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.
DR	PROPEP 1 113 BY SIMILARITY.
FT	CHAIN 114 266 INTERLEUKIN-1 BETA.
FT	CARBOHYD 58 58 POTENTIAL.
FT	SEQUENCE 266 AA; 30629 MW; 738323589 CRC32;
SO	
Query Match	17.2%; Score 223; DB 5; Length 266;
Best Local Similarity	37.1%; Pred. No. 6.50e-27;
Matches	33; Conservative 16; Mismatches 38; Indels 2; Gaps
Db	173 lgirdkngylscvkgdtdptllgleevd-pkvyppkrmekrfvkteikdtevesvlyp 231
QY	: : : : :
QY	86 LGTHGKMCLSCKVSGDETRLQLEAVNITDLSNRRKQDKRFARIRSDSGPTTSFESAACP 145
Db	232 nvyistshpeekpvflighfrg-gqditdf 259
QY	: : : : : :
QY	146 GWFLCTAMEADQPVSLTNMPDEGVMTKF 174
RESULT	9
ID	IL1B_PIG STANDARD; PRt; 267 AA.
AC	P26889;
DT	01-AUG-1992 (REL. 23, CREATED)
DT	01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
DT	01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE	INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN	IL1B.
OS	SUS SCROFA (PIG).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; ARTIODACTYLA.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 93314975.
RL	HUEFNER M.J., LIN G., SMITH D.M., MURTAUGH M.P., MOLITOR T.W.;
RL	GENE 129:285-289(1993).
CC	-!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC	THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC	MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC	IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC	IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE
CC	THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC	-!- SUBUNIT: MONOMER.
CC	-!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO
CC	ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC	-!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
CC	SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS
CC	SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC	SECRETORY PROTEINS.
CC	-!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC	EMBL; M86725; G184608; -.
DR	PIR; JN0724; JN0724.
DR	HSSP; P01584; I1B1.
DR	PROSITE; PS00253; INTERLEUKIN-1.
KW	CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.
FT	PROPEP 1 114 BY SIMILARITY.
FT	CHAIN 115 267 INTERLEUKIN-1 BETA.
FT	CARBOHYD 46 46 POTENTIAL.
FT	CARBOHYD 59 59 POTENTIAL.
SO	SEQUENCE 267 AA; 30404 MW; 5930DFAR CRC32:

EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
[1]
SEQUENCE FROM N.A.
MEDLINE: 96003435,
VILLINGER F.J., BRAR S.S., MAYNE A.E., CHIKKALA N., ANSARI A.A.;
J. IMMUNOL. 155:3946-3954(1995).
-!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
-!- SUBUNIT: MONOMER.
-!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO
ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
-!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS
SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
SECRETORY PROTEINS.
-!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
EMBL: U19853; G644824; -;
CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.
PROPEP 1 il6 BY SIMILARITY.
CHAIN 117 269 INTERLEUKIN-1 BETA.
SEQUENCE 269 AA; 30612 MW; 30E237F3 CRC32;
Query Match 15 6%; Score 202; DB 5; Length 269;
Best local Similarity 33.7%; Pred.No.2.39e-22;
Matches 31; Conservative 18; Mismatches 41; Indels 2; Gaps 2;

176 lglaknlylscvllkddkptlglesvdpkny-p-kkkmekrfvnklnnkiefesaqfp 234
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::
85 LGIHGGKCLSCVSGDETRLGLEAVNITDLENKRQDKRFARISDSGPTTSFESAACP 145
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::
235 nvyistsqaenmpvfvgtrg-gqditdfmq 265
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::
146 GWFLCTAMEADQPVSILTNPDEGVMTKFYQ 177
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 12
IL1B_HUMAN STANDARD; PRT; 269 AA.
AC PO1584;
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA) (CATABOLIN).
IL1B.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; PRIMATES.
[1]
SEQUENCE FROM N.A.
MEDLINE: 85088517.
AURON P.E., WEBB A.C., ROSENWASSER L.J., MUCCI S.F., RICH A.,
WOLFF S.M., DINARELLO C.A.;
PROC. NATL. ACAD. SCI. U.S.A. 81:7907-7911(1984).
[2]
SEQUENCE FROM N.A.
MEDLINE: 85240547.
MARCH C.J., MOSLEY B., LARSEN A., CERRETTI D.P., BRAEDT G., PRICE V.,
GILLIS S., HENNEY C.S., KRONHEIM S.R., GRABSTEIN K., CONLON P.J.,
HOPP T.P., COSMAN D.;
NATURE 315:641-647(1985).
[3]
SEQUENCE FROM N.A.
MEDLINE: 87040762.
CLARK B.D., COLLINS K.L., GANDY M.S., WEBB A.C., AURON P.E.;
NUCLEIC ACIDS RES. 14:7897-7914(1986).
[4]
SEQUENCE FROM N.A.
MEDLINE: 87248099.

DR		EMBL; M15330; G307045; -.	
DR	PIR;	A01848; ICHUIB.	
DR	PIR;	A25542; A25542.	
DR	PIR;	A29019; A29019.	
DR	PIR;	B27616; B27616.	
DR	PIR;	S19626; S19626.	
DR	PDB;	1IIB; 15-OCT-92.	
DR	PDB;	2IIB; 15-APR-92.	
DR	PDB;	3IIB; 15-APR-92.	
DR	PDB;	4IIB; 15-JUL-92.	
DR	PDB;	1HIB; 31-JAN-94.	
DR	MIM;	147720; -.	
DR	PROSITE;	PS00253; INTERLEUKIN_1.	
DR	CYTOKINE,	MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN;	
KW	3D-STRUCTURE.		
FFT	PROPEP	1	116
FFT	CHAIN	117	269
FFT	CAROHVD	123	123
FFT	CONFLICT	6	6
FFT	CONFLICT	20	20
FFT	CONFLICT	111	111
FFT	CONFLICT	177	177
FFT	CONFLICT	214	214
FFT	STRAND	121	128
FFT	TURN	129	130
FFT	STRAND	132	138
FFT	TURN	139	140
FFT	STRAND	141	147
FFT	TURN	148	150
FFT	STRAND	151	151
FFT	STRAND	158	162
FFT	STRAND	171	178
FFT	TURN	179	182
FFT	STRAND	183	190
FFT	TURN	191	192
FFT	STRAND	193	200
FFT	TURN	203	205
FFT	HELIX	213	215
FFT	STRAND	216	221
FFT	STRAND	226	230
FFT	TURN	234	235
FFT	STRAND	237	240
FFT	TURN	244	245
FFT	STRAND	246	247
FFT	STRAND	249	251
FFT	STRAND	259	259
FFT	STRAND	262	265
FFT	CONFLICT	6	6
SSQ	SEQUENCE	269 AA; 30747 MW; C858946 CRC32;	K -> E (IN REF. 2).
Query Match		15.4%; Score 200; DB 5; Length 269;	
Best Local Similarity		33.7%; Pred. No. 6.42e-22;	
Matches		31; Conservative 17; Mismatches 42; Indels 2; Gaps	
Ddb	176	Iglkknlylscvlkdxtqlqlesvdpkny-p-kkkmekrfvfkiefnnkfesagfp	234
QQY	86	LGIHGKMKCLSCVKSGDETRLQLAEAVNTIDLSNRKQDKRFARIRSDSGPTTSFESAACP	145
Ddb	235	nvyistsqaempvf1g9-tkgggdiftmq	265
QQY	146	GWLFCAMEADQPVSLTNMPDEGVNVTKFYFQ	177
RESULT 13			
ID	ILIB_FELCA	STANDARD;	PRT; 267 AA.
AC	F41687;		
DT	01-NOV-1995 (REL. 32; CREATED)		
DD	01-NOV-1995 (REL. 32; LAST SEQUENCE UPDATE)		

01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
IL1B.
GN
DE
OC EULIS SILVESTRIUS CATUS (CAT).
OC EKUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; CARNIVORA.
[1]
SEQUENCE FROM N.A.
RN RP
RC DANIEL S.L., BRENNER C.A., LEGENDRE A.M., SOLOMAN A., ROUSE B.T.;
CA SUBMITTED (XXX-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
RL
CC -! FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC -! SUBUNIT: MONOMER.
CC -! THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO
CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -! THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS
CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -! SIMILARITY: BELONGS TO THE IL-1 FAMILY.
DR EMBL; M92060; G402365; -
DR PROSITE; PS00253; INTERLEUKIN_1.
FW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.
KW PROEP 1 115 BY SIMILARITY.
FT CHAIN 116 267 INTERLEUKIN-1 BETA.
FT CARBOHYD 37 37 POTENTIAL.
FT CARBOHYD 58 58 POTENTIAL.
FT CARBOHYD 217 217 POTENTIAL.
SQ SEQUENCE 267 AA; 30361 MW; 0ECC9B96 CRC32;

Query Match 15.3%; Score 198; DB 5; Length 267;
Best Local Similarity 28.7%; Pred.No.1.72e-21;
Matches 41; Conservative 34; Mismatches 59; Indels 9; Gaps

Db 121 qdytfdrdisksivlsgsyelralhngqmqnqvffirmsfvhgseenskkipvvlckkn 180
QY 39 QAFRRIDWVKTKTYLRNN--OLVAGYLQGPNVNLEE--KIDVVPTEPHA--L--FLGTHGG 91
Db 181 nlylscvmkgdkptqlgmlid-pkvyppkkkmekrfvnfktnkgnvfessqfnpwviyt 239
QY 92 KNCLSVCVKSDEFRLQLEAVNIIDLSENRRQRFAIRSDSGPTTSFESACPGWFELCT 151
240 sqaeeapvflgn-tkgggqdtdf 261
QY 152 AMEAQPVSILTNPDEGVMTKF 174

RESULT 14
ID IL1B.RABIT STANDARD; PRT; 268 AA.
AC P14628;
DT 01-APR-1990 (REL. 14, CREATED)
DT 01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA) (LYMPHOCYTE PROLIFERATION
DN POTENTIATING FACTOR).
GN IL1B.
OS ORYCTOLAGUS CUNICULUS (RABBIT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; LAGOMORPHA.
[1]
SEQUENCE FROM N.A.
RN RP
RX MEDLINE; 89176242.
RA CANNON J.G., CLARK B.D., WINGFIELD P., SCHWEISSNER U., LOSBERGER C.,
RA DINARELLO C.A., SHAW A.R.;
RN J. IMMUNOL. 142:2299-2306(1989).
RL [2]
SEQUENCE FROM N.A.
RX MEDLINE; 88134238.

MORI S., GOTO F., GOTO K., OHKAWARA S., MAEDA S., SHIMADA K.,
YOSHINAGA M.;
BIOCHEM. BIOPHYS. RES. COMMUN. 150:1237-1243(1988).
[3]
RN RP
SEQUENCE FROM N.A.
MEDLINE; 89315718.
RX
RA YOUNG P.R., SYLVESTER D.;
PROTEIN ENG. 2:545-551(1989).
CC CC
-!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC CC
IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC CC
-!- SUBUNIT: MONOMER.
CC CC
-!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO
ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC CC
-!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS
SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
SECRETORY PROTEINS.
CC CC
-!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
EMBL; D21835; G452204; -;
DR DR EMBL; M26295; G516633; -;
DR DR PIR; A27714; A27714.
DR DR PIR; JU0082; JU0082.
DR DR PIR; A30584; A30584.
DR DR HSP; P01584; IHI8.
DR DR PROSITE; PS00253; INTERLEUKIN_1.
KW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.
FT PROPEP 1 116
FT CHAIN 117 268 INTERLEUKIN-1 BETA.
FFT CARBOHYD 58 58 POTENTIAL.
FFT CARBOHYD 251 251 POTENTIAL.
SQ SEQUENCE 268 AA; 30665 MW; E9C910FE CRC32;

Query Match 15.0%; Score 195; DB 5; Length 268;
Best Local Similarity 37.2%; Pred. No. 7.49e-21;
Matches 29; Conservative 16; Mismatches 32; Indels 1; Gaps

Ddb 175 lglrknlyscvmdkdtlqlgsvd-pnyrypkkmekrfvnfknlekdksaqfp 233
||| : : |||| : | |||| : : : ||| : : : |||| :
Qy 86 LGIHGKMCLSCVSGDETRLOEAVNITDLSENKRQDKRFAFIRSDDPTTSFESAACP 145

Ddb 234 nvyistsqteymvflgn 251
||| : : |||| : | |||| :
Qy 146 GWFLCTAMEADQPVLTN 163

RESULT 15
ID IL1B.CERTO STANDARD; PRT; 269 AA.
AC P46648;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS CERCOCEBUS TORQUATUS ATYS (RED-CROWNED MANGABEY) (SOOTY MANGABEY).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; PRIMATES.
RC [1]
RN
SEQUENCE FROM N.A.
RP TISSUE-BLOOD.
RX MEDLINE; 96003435.
RA VILLINGER F.J., BRAR S.S., MAYNE A.E., CHIKKALA N., ANSARI A.A.;
J. IMMUNOL. 155:3946-3954(1995).
CC CC
-!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC CC
IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIED AS ENDOGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC CC
-!- SUBUNIT: MONOMER.

CC -!- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -!- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 DR EMBL: U19837; G644792; -
 DR PROSITE; PS00253; INTERLEUKIN_1.
 KW CYTOKINE; MACROPHAGE; MITOGEN; INFLAMMATORY RESPONSE; PYROGEN.
 FT PROPEP 1 116 BY SIMILARITY.
 FT CHAIN 117 269 INTERLEUKIN-1 BETA.
 SQ SEQUENCE 269 AA; 30445 MW; F1397FAE CRC32;
 Query Match 14.2%; Score 184; DB 5; Length 269;
 Best Local Similarity 32.6%; Pred. NO. 1.57e-18;
 Matches 30; Conservative 18; Mismatches 42; Indels 2; Gaps 2;
 Db 176 lgikaknlylscvklkddkptlgiesvdpkayp-kkmekrfvfkieinnklecesadfp 234
 86 LGHHGKMCUSCVKSGDETRQLQLEAVNITDLSNRKQDKRFAFIRSDSGPTTSFESAACP 145
 235 nwyistsqaenmpvflggtgrg-gqditdftmq 265
 146 GWFLCTAMEADQPVSILNMPDEGVWTKFYEQ 177

Search completed: Thu Feb 19 10:11:16 1998
 Job time : 22 secs.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	579	100.0	579 143	A50279	Sequence 13 from Pate	0.00e+00
2	573	99.0	578 91	HSILIRAI1	H.sapiens mRNA for in	0.00e+00
3	474	81.9	474 143	A50276	Sequence 10 from Pate	0.00e+00
4	474	81.9	540 70	I09592	Sequence 3 from Pate	0.00e+00
5	474	81.9	1684 91	HSILIRAP	H.sapiens mRNA for IR	0.00e+00
6	474	81.9	1740 91	HSILIRA	H.sapiens mRNA for in	0.00e+00
7	472	81.5	600 70	I09594	Sequence 8 from Pate	0.00e+00
8	472	81.5	600 70	I08135	Sequence 3 from Pate	0.00e+00
9	471	81.2	602 99	HUMILIRAA	Human icIL-1ra mRNA,	0.00e+00
10	470	81.2	540 70	I09591	Sequence 1 from Pate	0.00e+00
11	469	81.0	534 99	HOMILRA	Human interleukin 1 r	0.00e+00
12	468	80.8	531 142	A50144	Sequence 1 from Pate	0.00e+00
13	468	80.8	531 142	A49726	Sequence 1 from Pate	0.00e+00
14	322	55.6	563 61	FIGIRAP	Sus scrofa (clone p03	7.53e-246
15	319	55.1	1594 61	RABILIRAI	Rabbit mRNA for inter	3.18e-243
16	319	55.1	1612 61	RABILIRAB	Rabbit interleukin 1	3.18e-243
17	317	54.7	574 61	S68977	sIL-1ra-interleukin-1	1.79e-241
18	296	51.1	542 111	S64082	interleukin 1 recepto	4.06e-223
19	296	51.1	1576 108	MUSILIRAA	Mouse interleukin 1 r	4.06e-223
20	296	51.1	1877 108	MUSILIRN	Mouse IL-1rn antagoni	4.06e-223
21	296	51.1	1940 108	MUSILIRA	Mus domesticus interl	4.06e-223
22	293	50.6	520 108	MUSILRA	M.musculus interleuki	1.69e-220
23	269	46.5	537 109	RATILRA	Rat interleukin 1 rec	5.32e-158
24	221	38.2	12565 137	HSILIRECA	H.sapiens gene for in	5.32e-158
25	221	38.2	12565 91	HSILIRECA	H.sapiens gene for in	5.32e-158
26	221	38.2	12565 9	HSILIRECA	H.sapiens gene for in	5.32e-158
27	186	32.1	270 70	I08134	H.sapiens gene for in	6.08e-128
28	186	32.1	270 70	I09593	Sequence 1 from Pate	6.08e-128
29	131	22.6	6350 108	MUSILIRN	Sequence 6 from Pate	1.92e-81
30	78	13.5	241 61	S68978	Mouse germline interl	2.73e-38
31	72	12.4	99 143	A50274	icIL-1ra-interleukin-	1.34e-33
32	37	6.4	42 143	A50272	Sequence 8 from Pate	4.89e-08
33	37	6.4	2172 91	HSICILIRA	H.sapiens IL-1ra gene	4.89e-08
34	32	5.5	465 67	A32116	Synthetic (126A1a,128	7.82e-05
35	32	5.5	986 68	E01591	CDNA encoding human I	7.82e-05
36	31	5.4	944 59	BOVILIBA	Bovine interleukin 1-	3.24e-04
37	31	5.4	944 59	BTILIBR	Bovine mRNA for inter	3.24e-04
38	31	5.4	1736 59	BOVILIB	Bovine interleukin 1-	3.24e-04
39	31	5.4	1750 69	I03510	Sequence 1 from Pate	3.24e-04
40	30	5.2	465 67	A32000	Synthetic IL-1 beta g	1.31e-03
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ALIGNMENTS

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NI e1039152
DT 07-MAR-1997 (Rel. 51, Created)
DE 07-MAR-1997 (Rel. 51, Last updated, Version 1)
DS Sequence 13 from Patent WO9612022.
KW
OS unidentified
OC unclassified
RN [1]
RP 1-579
RA Colotta F., Muzio M., Mantovani A.;
RT "INTRACELLULAR ISOFORM OF THE INTERLEUKIN-1 RECEPTOR
RL Patent number WO9612022-A/13, 25-APR-1996.
RL APPLIED RESEARCH SYSTEMS (NL).

W A S E R E H (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Feb 19 09:38:05 1998; MasPar time 625.32 Seconds
1315.209 Million cell updates/sec
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Perfect Score: 579
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Comp: GTCTTCTCGGAGCAGGAT.....AGTCTCTGCTCATCATG

Scoring table: TABLE default
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Nmatch STD : Dbase 0; Query 0

Searched: 430261 seqs, 710217276 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Statistics: Mean 10.706; Variance 5.142; scale 2.082

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NI e1039151
 DT 07-MAR-1997 (Rel. 51, Created)
 DT 07-MAR-1997 (Rel. 51, Last updated, Version 1)
 DE Sequence 10 from Patent WO9612022.
 KW
 OS unidentified
 OC unclassified.
 RN [1]
 RP 1-474
 RA Colotta F., Muzio M., Mantovani A.;
 RT "INTRACELLULAR ISOFORM OF THE INTERLEUKIN-1 RECEPTOR
 RT ANTAGONIST";
 RL Patent number WO9612022-A/10, 25-APR-1996.
 RL APPLIED RESEARCH SYSTEMS (NL).
 CC Other publication AD 3841795 960506
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 ACCESSION I09592
 NID 9587700
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

Unclassified.
 1 (bases 1 to 540)
 Hannon,C.H., Eisenberg,S.P., Thompson,R.C., Arend,W.p., Joslin,F.G.
 and Sommer,A.
 INTERLEUKIN-1 INHIBITORS
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 ACCESSION X53296
 NID g32578
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 SOURCE human.

ORGANISM Homo sapiens
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 Vertebrata; Euthera; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 1684)
 Carter,D.B., Delbel,M.R., Dunn,C.J., Tomich,C.S.C., Laborde,A.L.,
 Slightom,J.L., Berger,A.E., Bienkowski,M.J., Sun,F.F., McEwan,R.N.,
 Harris,P.K.W., Yem,A.W., Waszak,G.A., Chosay,J.G., Sieu,L.C.,
 Hardee,M.M., Zurcher-Neely,H.A., Reardon,I.M., Heinrikson,R.L.,
 Truesdell,S.E., Shelly,J.A., Eessalu,T.E., Taylor,B.M. and
 Tracey,D.E.

Purification, cloning, expression and biological characterization
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 Nature 344 (6267), 633-638 (1990)
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ACCESSION X52015
NID g32576
KEYWORDS interleukin 1 receptor antagonist.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1740)
AUTHORS Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Eisenberg, S. P., Evans, R. J., Arend, W. P., Verderber, E., Brewer, M. T.,
Hannum, C. H., and Thompson, R. C.
TITLE Primary structure and functional expression from complementary DNA
of a human interleukin-1 receptor antagonist
MEDLINE Nature 343 (6256), 341-346 (1990)
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DEFINITION Sequence 8 from Patent WO 8911540.
ACCESSION IO9594
NID g587702
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 600)
AUTHORS Hannon, C. H., Eisenberg, S. P., Thompson, R. C., Arend, W. P., Joslin, F. G.
and Sommer, A.
TITLE INTERLEUKIN-1 INHIBITORS
JOURNAL Patent: WO 8911540-A 8 30-NOV-1989;
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ACCESSION	M55646								
NID	9186291								
KEYWORDS	interleukin 1 receptor antagonist.								
SOURCE	Human epithelial/leukocyte, cDNA to mRNA.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
AUTHORS	Haskill, S., Martin, G., Van Le, L., Morris, J., Peace, A., Bigler, C.F., Hammerberg, C., Fong, S., Arend, W.P., Ralph, P. and Sporn, S.A.								
TITLE	cDNA cloning of an intracellular form of the human interleukin 1 receptor antagonist associated with epithelium								
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 88 (9), 3681-3685 (1991)								
MEDLINE	91219436								
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SOURCE	Unknown.								
ORGANISM	Unclassified.								
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AUTHORS	Hannum, C.H., Eisenberg, S.P., Thompson, R.C., Arend, W.P., Joslin, F.G. and Sommer, A.								
TITLE	Interleukin-1 inhibitors								
JOURNAL	Patent: EP 0343684-A1 3 29-NOV-1989;								
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Db	207	gacccaaatgcaatttagaagaaagatagatgtggtaccctattgagcctcatgctctg	266						
Qy	226	GGACCAAAATGTCATTTAGAGAAAAGATAGATGTGTTGCCATTCAGCTCATGCTCTG	285						
Db	267	ttcttgggaatccatgagggagatgtgctgtcctgtctgtcaggtctggtgatgagacc	326						

RESULT	11
LOCUS	HUMILRA 534 bp DNA PRI 04-FEB-1997
DEFINITION	Human interleukin 1 receptor antagonist (IL1RN) gene, complete cds.
ACCESSION	M63099
NID	g186385
KEYWORDS	interleukin 1 receptor antagonist.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS	Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 534)
TITLE	Eisenberg,S.P., Brewer,M.T., Verderber,E., Heimdal,P., Brandhuber,B.J. and Thompson,R.C. Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family: evolution of a cytokine control mechanism Proc. Natl. Acad. Sci. U.S.A. 88 (12), 5232-5236 (1991) 91271363
JOURNAL	Location/Qualifiers
MEDLINE	1..534
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Qy	166 GATGTTAACCAAGAAGACCTTCTATCTAGAGAACCAACTAGTTGCTGATATTGCAA 225
Dbb	184 ggaccaaattgcaatttagaagaaaagatagttgtgatacccattgagcctcatgctcg 243
Ov	226 GGACCAAAATGCTCAATTAGAGAAAAAGATAGTGTGTCACCATTCAGCCTCATGCTTG 285

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304	Db	agactccactgagggcaggttaacatcactgacctgagcgagaaacagaagcaggacaag	363
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364	Db	cgcttcgcttcatccgtccagacagtgcccccaccaccagtttttgagttctgcgcctgc	423
406	QY	CGTTTCGCTTCTATCGCTCAGACAGTGGCCACCACCACCACTTTTGAGTCTGCCGCTGC	465
424	Db	ccgggtgttctctgcacagcgatgggaagctgaccagcccgctcagcctcaccacaatg	483
466	QY	CCGGGTGTCTCTGTCACAGCGATGGAAGCTGACAGCCGCTCAGCCTCACCATAATG	525
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NI	e1039973		
DT	10-MAR-1997 (Rel. 51, Created)		
DT	10-MAR-1997 (Rel. 51, Last updated, Version 1)		
DE	Sequence 1 from Patent WO9609323.		
KW	Homo sapiens (human)		
OS	Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;		
OC	Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.		
RN	[1]		
RP	1-531		
RA	Borascchi D., Bossu P., Ruggiero P., Macchia G., Tagliabue A.,		
RA	Frigerio F., Grifantini R., Frascotti G., Grandi G.;		
RA	"IL-1 RECEPTOR ANTAGONISTS WITH ENHANCED INHIBITORY ACTIVITY";		
RL	Patent number WO9609323-A/1, 28-MAR-1996.		
RL	DOMPE SPA (IT).		
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FF		LEAVNITDLSENKODKRFARISDSGPTTSFESACPCWFLCTAMEADQPVSLTNMP	
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FF	sig_peptide	76..531	
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FF	mutation	/replace="CGC"	
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FF	mutation	400..402	
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FF		AMINOACID SUBSTITUTION AT THIS POSITION."	
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Best Local Similarity 100.0%; Pred. No. 0.00e+00;			
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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 QY 526 CCTGACGAAGCGCTCATGTCAACAAATCTACTTCCAGGAGGACGAG 573

RESULT 14
 LOCUS PIGIRAP 563 bp mRNA MAM 10-MAY-1996
 DEFINITION Sus scrofa (clone p0328w) IRAP1 mRNA, complete cds.
 ACCESSION L38849
 NID g1313894
 KEYWORDS IRAP1 gene; PCR.
 SOURCE Sus scrofa (strain crossbreed) (clone: p0328w) (tissue library: phage cDNA) lung cDNA to mRNA.

ORGANISM
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus.

REFERENCE
 1 (bases 1 to 563)
 Yin, J. and Murtaugh, M.P.
 TITLE Characterization of IRAP in morphine treated pig
 JOURNAL Unpublished (1995)
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Matches 396; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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 QY 166 GATGTTAACAGAAGACCCTTCTATCTGAGGAACAAACCACTAGTGTGCTGATCTGCAA 225
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 QY 346 AGACTCCAGCTGAGGAGCTTAACATCACTGACCTGAGCGAGAGAACAGAGGACAAG 405
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 QY 526 CCTGACGAAGCGCTCATGTGTCACCAAAATCTACTTCCAGGAGGACGAGTA 575

RESULT 15
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 DEFINITION Rabbit mRNA for interleukin 1 receptor antagonist, complete cds.
 ACCESSION D21832
 NID g425787
 KEYWORDS cytokine; interleukin 1 receptor antagonist; regulation of inflammation.
 SOURCE Oryctolagus cuniculus neutrophil cDNA to mRNA.
 ORGANISM Oryctolagus cuniculus
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE
 1 (bases 1 to 1594)
 Goto, F., Goto, K., Miyata, T., Ohkawara, S., Takao, T., Mori, S., Furukawa, S., Maeda, T., Iwanaga, S., Shimonishi, Y. and Yoshinaga, M.
 TITLE Interleukin-1 receptor antagonist in inflammatory exudate cells of rabbits. Production, purification and determination of primary structure
 JOURNAL Immunology 77 (2), 235-244 (1992)
 MEDLINE 93052512
 REFERENCE 2 (bases 1 to 1594)
 Goto, F.
 TITLE Direct Submission
 JOURNAL Submitted (28-OCT-1993) to the DDBJ/EMBL/GenBank databases.
 Fumimasa Goto, Kumamoto University School of Medicine, Department of Pathology, 2-2-1 Honjo, Kumamoto, Kumamoto 860, Japan
 (Tel:096-344-2111(ex.6291), Fax:096-372-6140)
 COMMENT Submitted (28-Oct-1993) to DDBJ by:
 Fumimasa Goto
 Department of Pathology
 Kumamoto University School of Medicine
 2-2-1 Honjo, Kumamoto
 Kumamoto 860
 Japan
 Phone: 096-344-2111 x6291
 Fax: 096-372-6140.
 Location/Qualifiers
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 /organism="Oryctolagus cuniculus"

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Matches 395; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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